

FIGURE 1B

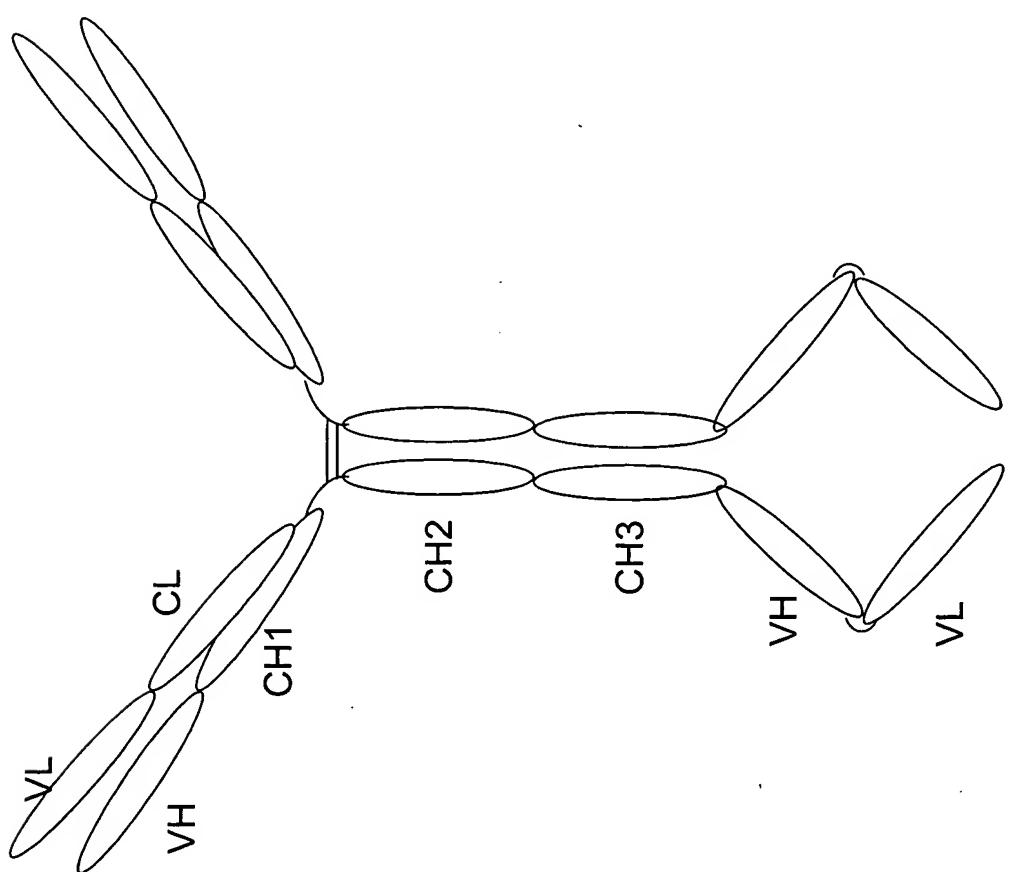


FIGURE 1A

Figure 2

→SP
M T V L A P A W S P T T Y L L L L L L S S G L S
0001 ATGACAGTGTGGCCAGCTGGAGCCAAACACCTATCTCCTCTGCTGCTGCTGAGCTGGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCTTCAACACAGCCCCATCTCCTCGACTTCGCTGTCAAATCCGTGAGCTGTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAGATTACCCAGTCACCGTGGCCTCAACCTCGAGGACGAGGAGCTCTGCGGGGGCTGGGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACTTTGTACCAAAATGTGCCTTCAGCCCCCCCCAGCTGCTTCGCTCGCCAGACC 0375

N I S R L L Q E T S E Q . L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGCAGGAGACCTCGAGCAGCTGGCGCTGAAGCCCTGGATCACTGCCAGAACCTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCCTGGAGCTGCAGTGTCAAGCCGACTCCTCAACCTGCCACCCCATGGAGTCCCCGGCCCTGGAG 0525

Flex←|
A T A P T A P
0526 GCCACAGCCCCGACAGCCCCG 0546

Figure 3

→SP
M T V L A P A W S P T T Y L L L L L L S S G L S
0001 ATGACAGTGCTGGCGCCAGCCTGGAGCCAACAACCTATCTCCTCCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCCTCAACACAGCCCCATCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCCTCAACCTGCAAGGACGAGGAGCTCTGCGGGGGCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTTGCTGGAGCC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAAACACGGAGATACTTGTCAACCAATGTGCCCTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCCTCTGCAGGAGACCTCGAGCAGCTGGTGGCCTGAAGCCCTGGATCACTGCCAGAACCTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCAAGTGTCAAGCCGACTCTCAACCCCTGGCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

FLex←→hinge
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGGAGCCAAATCTTGACAAAACTCACACATGCCACCGTGGCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCCCTGGGGGACCGTCAGTCCTCCCTCTCCCCCCTAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAGCCGGGAGGAGCAGTACAACAGCACGTACCGGTGGTCTGCGTCCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCAAAGCCAAGGGCAGCCCCGAGAACCCACAGGTGACACCCCTGCCCATCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCGGTCAAGCTGACCTGGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGTGCTGGACTCCGACGGCTTCTTCCCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCTTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←|
N H Y T Q K S L S L S P G K
1201 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAA

Figure 4

G G G G S G G G G S G G G G G S
GGCGGTGGAGGCTCTGGTGGAGGC GGTT CAGGAGGCGGTGGATCT

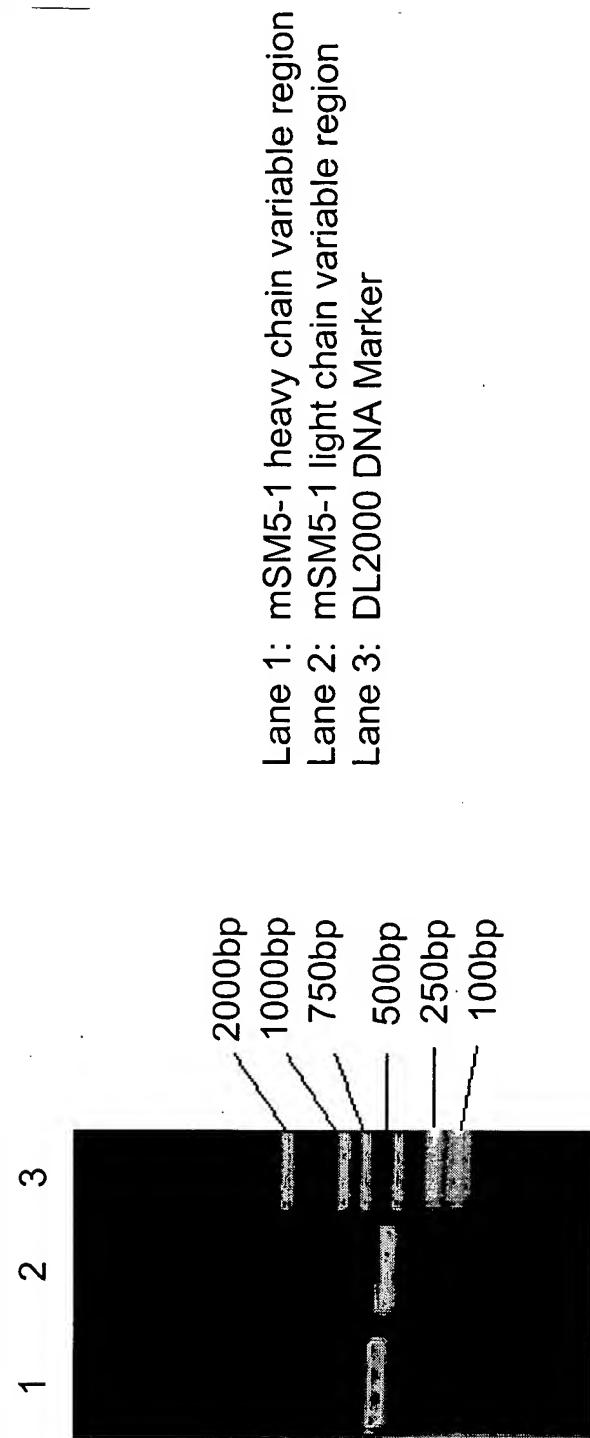


FIGURE 5

Figure 6

→SP SP←→VH
M E W S W I F L F L L S G T A G V H S E V
0001 ATCGCCGCCACCATGGATGGAGTTGGATTTCTCTCTCTGAGGAACTGCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGCTTCAGTGAAGATGTCCTGCAAGGCTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACGGGTGAAGCAGAAGCCTGGCAGGGCCTTGACTGGATTGGATATTTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAAGTACAATGAGAAGTTCAAAAGCAAGGCACACTGACTTCAGACAAATCCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGGTAC 0375
D W Y L D V W G A G T T V T V S S
0376 GACTGGTATTAGATGTCCTGGGCGCAGGGACACGGTACCGTCTCC 0426

Figure 7

→SP
M E S
0001 ATCATCACCAAGAACAGCTTACGAGCAGACCGCCAGACAGCTCACAGGGATCAAGCTGCCACCATGGAAATCA 0075
Q T Q V F L S L L L W V S G T C G N I M M T Q S P
0076 CAGACTCAGGCTCTCTCTGCTGCTGGTATCTGGTACCTGTGGAACATTATGATGACACAGTCGCCA 0150
S S L A V S A G E K V T M S C K S S Q S V L Y S S
0151 TCATCTCTGGCTGTCTGCAGGAGAAAGGTCACTATGAGCTGTAAGTCCAGTCAAAGTGTAACTACAGTTCA 0225
N Q K N Y L A W Y Q Q K P G Q S P K L L I Y W A S
0226 AATCAGAAGAAACTACTGGCTGGTACCGAGAAACCAAGGGCAGTCTCTAAACTGCTGATCTACTGGCATCC 0300
T R E S G V P D R F T G S G S G T D F T L T I S S
0301 ACTAGGGAAATCTGGTGTCCCTGATCGCTCACAGGCAGTGGATCTGGGACAGATTACTCTTACCATCAGCAGT 0375
V Q A E D L A V Y Y C H Q Y F S S Y T F G G G T K
0376 GTACAAGCTGAAGACCTGGCAGTTTATTACTGTCATCAATTTCTCTCATACACGTTGGAGGGGACCAAG 0450
V_L ← |
L E I K R
0451 CTGGAAATAAGCGG 0465

Figure 8

SP←|→VH
 M E W S W I F L F L L S G T A G V H S E V 0075
 0001 ATCGCCGCCACCATGGAATGGAGTGGATATTCTCTTCTCAGGAACCTGCAGGTCCTCACTCTGAGGTC 0075
 Q L Q Q S G P E L V K P G A S V K M S C K A S G Y 0076
 0076 CAGCTGCAGCAGCTGGACCTGAGCTGGTAAAGGCTGGGCTTCAGTGAAGATGCTCTGCAAGGCTCTGGATAC 0150
 T F T S Y V M H W V K Q K P G Q G L D W I G Y I V 0151
 0151 ACATCTACTGATGTATGCACTGGGTGAAGCAGAAGCCTGGCAGGGCTTGAAGTGGATTGGATATATTGTT 0225
 P Y N D G T K Y N E K F K G K A T L T S D K S S S 0226
 0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTCAAAGGCAAGGCCACACTGACTTCAGACAAATCTCCAGC 0300
 T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y 0301
 0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGGCTCTATTATTGTCACGGTAGTAGGTAC 0375
 VH←|→CH
 D W Y L D V W G A G T T V T V S S A S T K G P S V 0376
 0376 GACTGGTATTAGATGTCGGGGCGCAGGGACCAAGGTACCGTCTCCTCAGCTAGCACCAAGGGCCATCGTC 0450
 F P L A P S S K S T S G G T A A L G C L V K D Y F 0451
 0451 TTCCCCCTGGCACCCCTCCCAAGAGCACCTCTGGGGCACAGGGCCCTGGGCTGGCTGGTCAAGGACTACTTC 0525
 P E P V T V S W N S G A L T S G V H T F P A V L Q 0526
 0526 CCCGAACCGGTGACGGTCTTGGAACTCAGGCCCTGACCAGCGCGTGCACACCTTCCGGCTGTCCTACAG 0600
 S S G L Y S L S S V V T V P S S S L G T Q T Y I C 0601
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGGTCCCTCAGCAGCTGGCACCCAGACCTACATTCG 0675
 N V N H K P S N T K V D K K V 0676
 0676 AACGTGAATCACAAGGCCAGCAACACCAAGGTGGACAAGAAAGTGGTAGAGAGGCCAGCACAGGGAGGG 0750
 0751 TCTGGCTGAAGCAGGCTCAGCGCTCTGGCTGGACGCATCCGGCTATGGCAGCCCAGTCAGGGCAGCAAGGCA 0825
 0826 GGCCCCGTCTGCCTCTCACCCGAGCCTCTGCCGCCACTCATGCTCAGGGAGAGGGCTCTGGCTTTTC 0900
 0901 CCAGGCTCTGGGAGGACAGGCTAGGTGCCCCCTAACCCAGGCCGACACAAAGGGCAGGTGCTGGCTCAC 0975
 0976 ACCTGCCAAGAGCCATATCGGGAGGACCCCTGCCCTGACCTAACCCCAACCCAAAGGCCAAACTCTCCACTCC 1050
 E P K S C D 1051
 1051 TCAGCTGGACACCTTCTCTCCCAGATTCAGTAACCTCCAAATCTCTCTGAGACCCAAATCTGTGA 1125
 K T H T C P P C P 1126
 1126 CAAAACTCACACATGCCAACCGTGCCAGGTAAAGCCAGGCCAGGCCCTCGCCCTCCAGCTCAAGGGGGACAGGTG 1200
 A P 1201
 1201 CCCTAGAGTAGCCCTGCATCCAGGGACAGGCCAGGCCGGTGCTGACACGTCCACCTCCATCTTCCCTCAGCAC 1275
 E L L G G P S V F L F P P K P K D T L M I S R T P 1276
 1276 CTGAACCTCTGGGGGACCGTCAGTCTCTCTTCCCCCAAACCCAGACCCCTCATGATCTCCGGACCC 1350
 E V T C V V V D V S H E P E V K F N W Y V D D G V 1351
 1351 CTGAGGTCACATGCCGGTGGACGTGAGGCCAGGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGGACGGCG 1425
 E V H N A K T K P R E E Q Y N S T Y R V V V S V L T 1426
 1426 TGGAGGTGCATAATGCCAAGACAAGGCCGGGAGGACAGTACACAGCACGTACCGGGTGGCTGCGCTCTCA 1500
 V L H Q D W L N G K E Y K C K V S N K A L P A P I 1501
 1501 CGCTCTGCCACAGGACTGGCTGAATGCCAAGGAGTACAAGTGAAGGTCTCCAACAAAGGCCCTCCAGCCCCCA 1575
 E K T I S K A K 1576
 1576 TCGAGAAAACCATCTCAAAGCCAAGGTGGACCCGTGGGGTGGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
 G Q P R E P Q V Y T 1651
 1651 CCACCCCTCTGCCCTGAGAGTGAACCGCTGTACCAACCTCTGCTCACAGGGCAGGCCAGAACACAGGTGTACA 1725
 L P P S R D E L T K N Q V S L T C L V K G F Y P S 1726
 1726 CCCTGCCCTCATCCCGGATGAGCTGACCAAGAACCCAGGTGACCTGCTGGTCAAAGGCTCTATCCCA 1800
 D I A V E W E S N G Q P E N N Y K T T P P V L D S 1801
 1801 GCGACATGCCGGTGGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCAACGCCCTCCCGTGTGGACT 1875
 D G S F F L Y S K L T V D K S R W Q Q G N V F S C 1951
 1951 CGCAGGGCTCTTCTCTACAGCAAGCTACCCGTGACAAGAGCAGGTGGCAGCAGGGAAACGTCTCTCAT 2025
 S V M H E A L H N H Y T Q K S L S L S P G K STOP 1951
 1951 GCTCCCTGATGCAATGAGGCTCTGCCACACCAACTACACCGAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA 2021

Figure 9

0001 ATCATCACAGAACAGCTTACGAGCAGACGCCAGACAGCTCACAGGGATCAAGCTTGCAGGCCACCATGGAATCA 0075
0076 Q T Q V F L S L L L W V S G T C G N I M M T Q S P
0076 CAGACTCAGGTCTTCCCTCCCTGCTGCTCTGGTATCTGGTACCTGTGGAACATTATGATGACACAGTCGCCA 0150
0151 S S L A V S A G E K V T M S C K S S Q S V L Y S S
0151 TCATCTCTGGCTGTGCTGCAGGAGAAAAGGTCACTATGAGCTGAAGTCCAGTCAAAGTGTGTTATACAGTTCA 0225
0226 N Q K N Y L A W Y Q Q K P G Q S P K L L I Y W A S
0226 AATCAGAAGAACTACTTGGCTGGTACCAAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCC 0300
0301 T R E S G V P D R F T G S G S G T D F T L T I S S
0301 ACTAGGAAATCTGGTGTCCCTGATCGCTCACAGGCAGTGGATCTGGACAGATTACTCTTACCATCAGCAGT 0375
0376 V Q A E D L A V Y Y C H Q Y F S S Y T F G G G T K
0376 GTACAAGCTGAAGACCTGGCAGTTTATTACTGTCAATATTCTCCTCATACACGTCGGAGGGGGACCAAG 0450
0451 V_L ← | → C_L
0451 L E I K R T V A A P S V F I F P P S D E Q L K S G
0451 CTGGAAATAAAGCGGACTGTGGCTGCACCATCTGTCTTACATCTCCGCATCTGATGAGCAGTTGAAATCTGGA 0525
0526 T A S V V C L L N N F Y P R E A K V Q W K V D N A
0526 ACTGCCTCTGGTGTGCTGCTGAAATAACTCTATCCAGAGAGGCAAAAGTACAGTGAAGGTGGATAACGCC 0600
0601 L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0601 CTCCAATCGGTAACCTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0675
0676 L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0676 CTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCTGAGCTG 0750
0751 P V T K S F N R G E C Stop
0751 CCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAG 0786

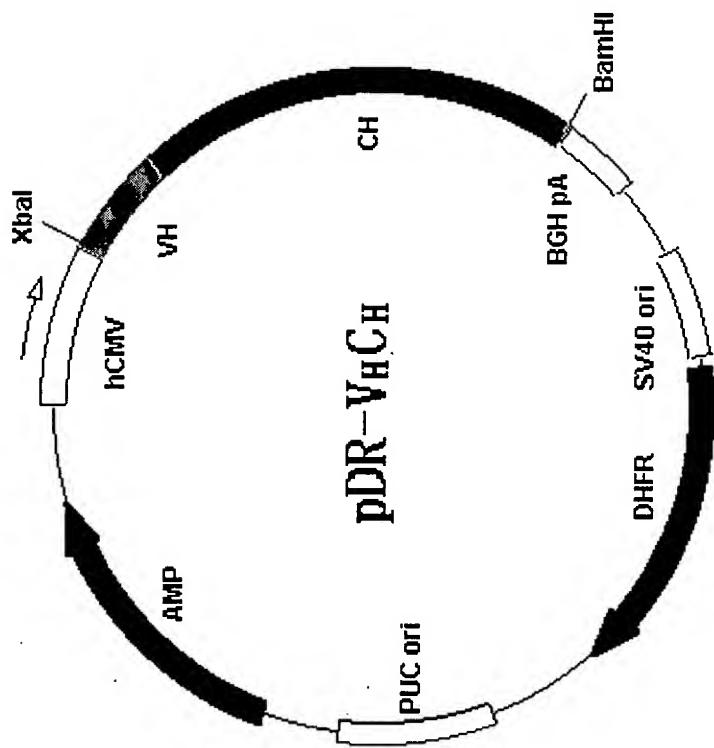


Figure 10

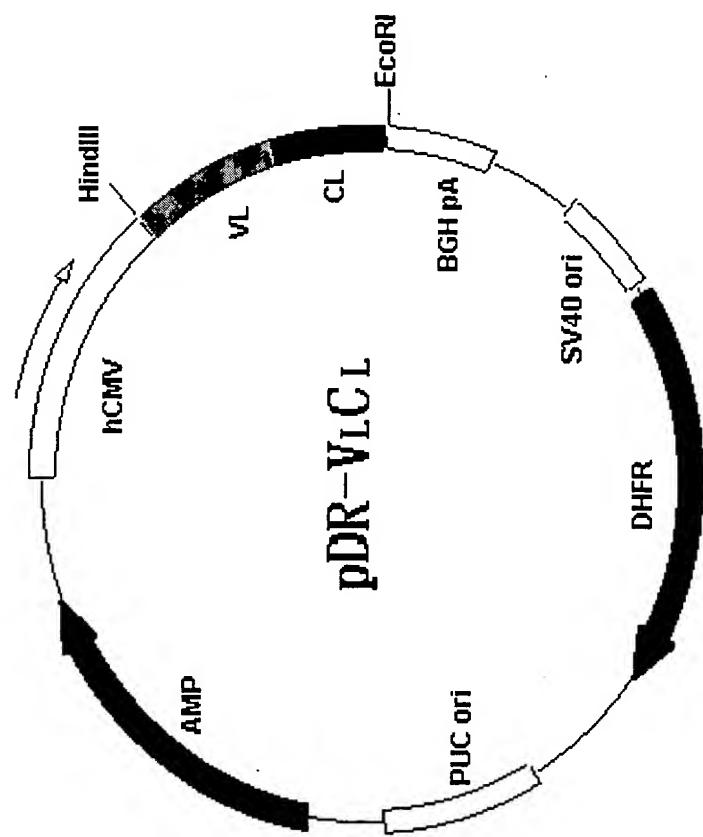


Figure 11

Figure 12

→SP SP←→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTGTTGTCACTGAGGTGTCCACTCCCAGGTG 0075

Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCAGTCAGCTGGCGGTGGAGTGGTCCAGCCCGCCGCAGCCTGAGGCTGTCCCTGCAAGGCATCTGGCTAC 0150

T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACCAAGCTACGTGATGACATGGGTGCGCAAGCCCCGGAAAGGGCCTCGAATGGATTGGCTACATTGTG 0225

P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAAGTCA 0300

T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTGCCTGAGGACACCGCCGTATACTATTGTGTGCGCGCAGCCGTTAC 0375

D W Y L D Y W G Q G T P V T V S S z
0376 GACTGGTACTTGGACTACTGGGGCCAAGGCACCTCCAGTCACCGTCTCCTCT 0426

Figure 13

|→SP

M D F Q V

0001 GAGCATTACCGGCCATACTCATCACCATCCCAGGATATCTCTAGAAAGCTTGCCGCCACCATGGATTTCAAGTG 0075

SP←|→V_L

0076 CAGATTTAGCTTCCTGCTAACAGTCAGTCAGTCATAATGTCCAGAGGAACATCATGATGACTCAGAGCCCA 0150

0151 TCCAGCTTGAGCGCATCAGTAGGCGACCGCGTAACGATCACTTGCAAATCCTCTCAGTCAGTATTGACTCCAGC 0225

0226 AACCAAGAAACTACCTGGCGGATATCAGCAGACTCCCGCAAAGCCCCAAAGTTGCTGATTATTGGGCTCC 0300

0301 ACGCAGCTGGCGAGTCAGCTGGCGTGCCATCACGCTTACAGCGGAGCAGGGTCCGGTACAGATTACAGTTACCATTTAGCAGT 0375

0376 CTGCAGCCTGAGGACATAGCCACCTACTACTGTACCAGTACTTTAGTCCTACACTTTGGCCAGGAACTAAA 0450

V_L←|

0451 CTGCAGATTACTCGA 0465

Figure 14

SP \leftarrow →VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTCGGTGTGGACCTTGCTATTCCCTGTTGCACTGAGGTGTCCACTCCAGGTG 0075

Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCAGTCAGCTGGCGTGGAGTGGTCCAGGCCGCCAGCCTGAGGCTGTCTGCAAGGCATCTGGTAC 0150

T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACCAAGCTACGTGATGACATGGGTGCGCAAGCCCCGGAAAGGGCTCGAATGGATTGGCTACATTGTG 0225

P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAAGTCA 0300

T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTGCCTGAGGACACCGCCGTATACTATTGTGTGCGCAGGCCGTAC 0375

VH \leftarrow →CH
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTGGACTACTGGGCAAGGCAGTCAGCTCAGCTCTGCTAGCACCAGGGCCATCGGTC 0450

F P L A P S S K S T S G G T A A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCCTCTCAAGAGCACCTCTGGGGCACAGGGCCCTGGCTGCTGGTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACCTCAGGCGCCCTGACCAGGGCGTGCACACCTCCGGCTGCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGGTGAAGAGGCCAGCACAGGGAGGGAGGTG 0750

0751 TCTGCTGGAAAGCAGGCTCAGCGCTCTGGCTGGAGCAGTCAGCTCCGGTATGAGGCCAGTCAGGGCAGGCA 0825

0826 GGCCCCGCTGCTGCCTCTCACCCGGAGCCCTGCCCCACTCATGCTCAGGGAGAGGGTCTCTGGCTTTTC 0900

0901 CCAGGCTCTGGGAGGCAACAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAGGGCAGGTGCTGGCTCAG 0975,

0976 ACCTGCCAAAGAGCCATATCCGGAGGACCCCTGCCCCCTGACCTAACGCCACCCAAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
1051 TCAGCTCGGACACCTTCTCTCCCTCCAGATTCCAGTAACCTCCAAATCTCTCTCTGCAGAGGCCAAATCTGTGA 1125

K T H T C P P C P
1126 CAAACTCACACATGCCACCGTGCCAGGTAAAGCCAGGCCAGGCCTGCCCTCCAGCTCAAGGCCAGGGACAGGTG 1200

A P
1201 CCCCTAGAGTAGGCTGCATCCAGGGACAGGCCAGGCCAGGGTGTGACAGTCCACCTCCATCTCTCCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCCTCTCTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCC 1350

E V T C V V V W D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGACGTGAGGCCAGAACCTGAGGTCAAGTCACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGATAATGCCAAAGACAAGGCCGGAGGAGCAGTACAACAGCACGCTACGGGTGGTCTGGCTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575

E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGGTGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGG 1650

G Q P R E P Q V Y T
1651 CCACCCCTCTGGCTGAGAGTGACCGCTGACCAACCTCTGCTACAGGGCAGCCCCAGAACACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCATCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACCTGCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCCGTGGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCCACGCCCTCCGTGCTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCTCTCAT 1950

S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCACTGGCTCTGCACAAACCAACTACACGCAAGAGCAGCCTCTCCCTGCTCCCGTAAATGA 2021

Figure 15

|→SP

M D F O V

0001 GAGCATTACCGGCCATACTCATCACCATCCCAGGATATCTCTAGAAAGCTTGCCGCCACCATGGATTTCAAGTG 0075

SP←|→V_L

Q I F S F L L I S A S V I M S R G N I M M T Q S P
0076 CAGATTTCAGCTTCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGAAACATCATGATGACTCAGAGCCCA 0150

S S L S A S V G D R V T I T C K S S Q S V L Y S S
0151 TCCAGCTTGAGCGCATCAGTAGGGCACCGCTAACGATCAGTCATAATGTGCTCAGTCAGTATTGACTCCAGC 0225

N Q K N Y L A W Y Q Q T P G K A P K L L I Y W A S
0226 AACCCAGAAGAACTACCTGGCGGATATCAGCAGACTCCCGCAAAGCCCCAAAGTTGCTGATTTATTGGGCTCC 0300

T R E S G V P S R F S G S G S G T D Y T F T I S S
0301 ACAGCGCGAGTCGGCGTGCATCACGCTTACGGCAGCGGGTCCGGTACAGATTACGTTACGTTACGAGT 0375

L Q P E D I A T Y Y C H Q Y F S S Y T F G Q G T K
0376 CTGAGCCTGAGGACATAGCCACCTACTGTACCGACTACTTACGTTACGTTACGTTACGTTACGTTACGAGT 0450

V_L←|→C_L

L Q I T R T V A A P S V F I F P P S D E Q L K S G
0451 CTGCAGATTACTCGAACCTGTGGCTGCACCATCTGCTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGA 0525

T A S V V C L L N N F Y P R E A K V Q W K V D N A
0526 ACTGCCTCTGTTGTGCTGCTGAATAACTTCTATCCCGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCC 0600

L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0601 CTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGCACGACAGCACCTACAGCCTCAGCAGCACC 0675

L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0676 CTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTGAGCTCG 0750

P V T K S F N R G E C Stop
0751 CCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAG 0786

Figure 16A

Figure 16A displays a sequence of amino acids, likely a fusion protein, with various domains and signal peptides. The sequence is organized into several sections, each starting with a signal peptide (SP) or a domain (VH, CH, FLEX) and ending with a domain (VH, CH, FLEX) or a signal peptide (SP). The sequence is as follows:

SP \rightarrow SP
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATCCTGTTGTCAGTAAC TG CAGGTGTCCACTCCAGGTG 0075

Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCAGTCTGGCGGTGGACTGGTCCAGCCGGCCAGCCTGAGGCTGTCCGTCAAGGCATCTGGCTAC 0150

T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACCAAGCTACGTGATGACATGGTGCGCCAAAGCCCCGAAAGGGCTCGAATGGATTGGCTACATIGTG 0225

P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAAGTCA 0300

T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCCCAAATGGACAGCTTGCGTCCAGAGGACACCGCCGTATACTATTGTGTGCGCAGGCCGTTAC 0375

VH \leftarrow CH
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTGGACTACTGGGCAAGGCACTCCAGTCACCGTCTCCGTGCTAGCACCAGGACAGGGCCATGGTC 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCCTCCAAAGGCACCTCTGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTCTTGGAACTCAGGCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCCCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCACAAACCAAGGTGACAAGAAAGTTGGTAGAGGGCAGCACAGGGAGGGGGTG 0750

0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGCTGGACCGCATCCGGTATGCAGCCCAAGTCCAGGGCAGCAAGGCA 0825

0826 GGCCCCGCTCTGCCCTCTCACCCGGACCTCTGCCGCCACTCATGGTCAGGGAGAGGGCTCTGGCTTTTC 0900

0901 CCAAGGCTCTGGGAGGGCACAGGTAGGTGCCCTAACCCAGGGCTGCACACAAGGGCAGGTGCTGGCTCAG 0975

0976 ACCTGCCAAAGAGCCATATCGGGAGGACCTGCCCTGACCTAACCCACCCAAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
1051 TCAGCTCGGACACCTTCTCTCCTCCAGATTCCAGTAACCTCCAAATCTCTCTCTGCAAGGCCAAATCTGTGA 1125

K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCCAGGTAAAGCCAGCCCAGGCCTGCCCTCCAGCTCAAGGGGACAGGTG 1200

A P
1201 CCCCTAGAGTAGGCTGCATCCAGGGACAGGCCCCAGGCCGGTGTGACAGTCCACCTCCATCTCTCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCTGGGGGACCGTCAGTCTCTCTTCCCTAACCCAAAGGACACCCCTCATGATCTCCGGACCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGGTACATCGTGGTGGACGTGAGGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCTAAATGCCAAGACAAGGCCGGGAGGAGCAGTACAACAGCAGCTACCCGGTGGTCTGCGTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCCTGACCCAGGACTGGCTGAATGCCAAGGAGTACAAGTCAAGGTCTCCAACAAGCCCTCCAGCCCCCA 1575

E K T I S K A K
1576 TCGAGAAAACCATCTCAAAGCCAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGCTCGGC 1650

G Q P R E P Q V Y T
1651 CCACCCCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGCTACAGGGCAGCCCGAGAACACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCGCCCATCCGGATGAGCTGACCAAGAACCGTACGCTGACCTGCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCCGTGGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCACGCCCTCCGTGCTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCCCTCTCTACAGCAAGCTACCGTGGACAGAGCAGGTGGCAGCAGGGAAACGTCTCTCAT 1950

S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGATGAGCTCTGCACACCAACTACACCGAGAACAGGCTCTCCGTCTCCGGTAAACCCAGG 2025

CH \leftarrow FLex

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCCTCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCTCCAACCTGCAGGACGAGGAGCTCGCGGGGCCCTGCGCGCTGGTCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTGTACCAAAATGTGCCTTCAGCCCCCCCCAGCTGCTTCGCTTGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCAGAACCTCTCCGGTGCC 2400

E L O C O P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTCAAGCCCCACTCCTCAACCCCTGCCACCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 16B

Figure 17A

Figure 17A displays a sequence of amino acids (SP) and nucleotides (VH) for a bifunctional fusion protein. The sequence is organized into several sections, each starting with a leader sequence (SP or VH) and ending with a linker sequence (Linker). The sections are separated by vertical lines with arrows pointing to the right.

SP Leader: M D W V W T L L F L L S V T A G V H S Q V

SP Sequence: 0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCCTGTTGTCAGTAAC TG CAGGTGTCCACTCCCAGGTG 0075

VH Leader: Q L V Q S G G G V V Q P G R S L R L S C K A S G Y

VH Sequence: 0076 CAGCTGGTGCAGTCTGGCGGTGGAGTGGTCCAGCCCGGCCAGCCTGAGGCTGTCCCTGCAAGGCATCTGGCTAC 0150

SP Leader: T F T S Y V M H W V R Q A P G K G L E W I G Y I V

SP Sequence: 0151 ACCTTCACCCAGCTACGTGATGACATGGGTGGCCAAGCCCCGGAAAGGGCCTCGAATGGATTGGCTACATTGTG 0225

VH Leader: P Y N D G T K Y N E K F K G R F T I S S D K S K S

VH Sequence: 0226 CCTTATAATGACGGTACTAAGTACAATGAAAGTTCAAGGCAGATTACAATATCAAGTGACAAGAGCAAGTC 0300

SP Leader: T A F L Q M D S L R P E D T A V Y Y C A R G S R Y

SP Sequence: 0301 ACCGCATTCTCCAAATGGACAGCTTGGCTCCAGAGGACACCGCCGTATACTATTGTGTGCGCGCAGCCGTTAC 0375

VH Leader: D W Y L D Y W G Q G T P V T V S S A S T K G P S V

VH Sequence: 0376 GACTGGTACTGGACTACTGGGGCCAAGGCACCTCCAGTCACCGTCTCCTGCTAGCACCAGGGCCATCGGTC 0450

SP Leader: F P L A P S S K S T S G G T A A A L G C L V K D Y F

SP Sequence: 0451 TTCCCCCTGGCACCCCTCCAAGAGCACCTCTGGGGCAACAGCGCCCTGGGCTGCGCTGGTCAAGGACTACTTC 0525

VH Leader: P E P V T V S W N S G A L T S G V H T F P A V L Q

VH Sequence: 0526 CCCGAACCGGTGACGGTGTCTGGAAACTCAGGCGCCCTGACCAGCGGGTGCACACCTTCCGGCTGCTACAG 0600

SP Leader: S S G L Y S L S S V V T V P S S S L G T Q T Y I C

SP Sequence: 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGGTGGCTCCAGCAGCTGGGACCCAGACCTACATCTGC 0675

VH Leader: N V N H K P S N T K V D K K V

VH Sequence: 0676 AACGTGAATCACAGCCAGAACACCAAGGTGGACAAGAAAGTTGGTGAAGGGCAGCACAGGGAGGGAGGGTG 0750

SP Leader: TCTGCTGGAAAGCAGGCTCAGCGCTCTGCCTGGACGCATCCGGCTATGCAGCCCAAGTCAGGGCAGCAAGGCA 0825

SP Sequence: 0751 0826 GGCCCCGCTCTGCCCTCTCACCCGGAGCCTCTGCCGCCCTGACACAAAGGGCAGGTGCTGGCTTTTC 0900

VH Leader: 0901 CCAGGCTCTGGGAGGGCAGGGCTAGGTGCCCCTAACCCAGGCCCTGACACAAAGGGCAGGTGCTGGCTCAG 0975

VH Sequence: 0976 ACCCTGCCAACAGGCCATATCCGGGAGGACCCCTGCCCTGACCTAACCCCAAGGCCAACCTAACATCTCC 1050

SP Leader: E P K S C D

SP Sequence: 1051 TCAGCTGGACACCTCTCTCCTCCAGTAACTCCAACTCTCTCTCTGCAAGGCCAAATCTGTGA 1125

VH Leader: K T H T C P P C P

VH Sequence: 1126 CAAACTCACACATGCCACCGTGCCCAGGTAAAGCCAGCCAGGCCCTGCCCTCCAGCTCAAGGGGGACAGGTG 1200

SP Leader: A P

SP Sequence: 1201 CCCCTAGAGTAGCCCTGCATCCAGGGACAGGCCAGGGCTGCTGACACGGTCCACCTCCATCTCTCAGCAC 1275

VH Leader: E L L G G P S V F L F P P K P K D T L M I S R T P

VH Sequence: 1276 CTGAACTCTGGGGGACCGTCAGTCCTCTCCCCAAAACCAAGGACACCCATGATCTCCGGACCC 1350

SP Leader: E V T C V V V D V S H E P E V K F N W Y V D D G V

SP Sequence: 1351 CTGAGGTCACATCGCTGGTGGTGACGTGAGCCACAGCCCTGAGGTCAAGTCACTGGTACGTGGACGGCG 1425

VH Leader: E V H N A K T K P R E E Q Y N S T Y R V V S V L T

VH Sequence: 1426 TGGAGGTGCTATAGCACAGAACAGCCGGGGAGGAGCAGTACAACAGCACGTCACGGGGTGGCTGCGTCTCA 1500

SP Leader: V L H Q D W L N G K E Y K C K V S N K A L P A P I

SP Sequence: 1501 CCGCTCTGACCCAGACTGGCTGAATGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCA 1575

VH Leader: E K T I S K A K

VH Sequence: 1576 TCGAGAAAACCATCTCCAAAGCCAAGGTGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGCTCGGC 1650

SP Leader: G Q P R E P Q V Y T

SP Sequence: 1651 CCACCCCTCTGCCCTGAGAGTGACCGCTGACCAACCTCTGCTACAGGGCAGGCCAGAACACAGGTGTACA 1725

VH Leader: L P P S R D E L T K N Q V S L T C L V K G F Y P S

VH Sequence: 1726 CCCTGCCCTCATCCGGATGAGCTGACCAAGAACAGGTACAGCTGACCTGCCCTGGTCAAAGGCTTCTATCCCA 1800

SP Leader: D I A V E W E S N G Q P E N N Y K T T P P V L D S

SP Sequence: 1801 GCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAACGCCCTCCGTGCTGGACT 1875

VH Leader: D G S F F L Y S K L T V D K S R W Q Q G N V F S C

VH Sequence: 1876 CCGACGGCTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCCTCTCAT 1950

Linker Leader: S V M H E A L H N H Y T Q K S L S L S P G K G G G

Linker Sequence: 1951 GCTCCGTGATGCATGAGGCTCTGCACAAACCAACTACACCGCAGAAGAGCCTCTCCCTGCTCCCGTAAAGGCAGGTG 2025

Linker↔→FLex

G S G G G G S G G G G S T Q D C S F Q H S P I S S

2026 GAGGCTCTGGTGGAGGCGGTTCAAGGAGGCGGTGGATCTACCCAGGACTGCTCCCTCCAACACAGCCCCATCTCCT 2100

D F A V K I R E L S D Y L L Q D Y P V T V A S N L

2101 CCGACTTCGCTGTCAAATCCGTAGCTGTCTGACTACCTGCTTCAGATTACCCAGTCACCGTGGCTCCAACC 2175

Q D E E L C G G L W R L V L A Q R W M E R L K T V

2176 TGCAGGACGAGGAGCTCTGGGGGGCTCTGGGGCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250

A G S K M Q G L L E R V N T E I H F V T K C A F Q

2251 TCGCTGGTCCAAGATGCAAGGCTTGCTGGAGCGGTGAACACGGAGATACTTTGTACCCAAATGTGCCCTTC 2325

P P P S C L R F V Q T N I S R L L Q E T S E Q L V

2326 AGCCCCCCCCCAGCTGCTTCGCTTCGAGACCAACATCTCCCGCTCCCTGCAGGAGACCTCCGAGCAGCTGG 2400

A L K P W I T R Q N F S R C L E L Q C Q P D S S T

2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACCTCTCCCGGTGGAGCTGCAGTGTCAAGCCGACTCCTCAA 2475

L P P P W S P R P L E A T A P T A P STOP

2476 CCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 17B

Figure 18A

→SP
 M T V L A P A W S P T T Y L L L L L L L S S G L S
 0001 ATGACAGTGCCTGGCGCCAGCCTGGAGCCAAACACTATCTCCCTCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→Flex
 G T Q D C S F Q H S P I S S D F A V K I R E L S D
 0076 GGGACCCAGGACTGCCTCCAACACAGCCCCATCTCCCTGGACTTCGCTGTCAAATCCGTGAGCTGTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
 0151 TACCTGCTTCAGATTACCCAGTCACCGTGGCTCAACCTGCAGGACGAGGAGCTCTGCGGGGCTCTGGCG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
 0226 CTGGTCCCTGGCACAGCGCTGGATGGAGCGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTTGCTGGAGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
 0301 GTGAACACGGAGATACACTTGTCAACCAATGTGCCCTTCAGCCCCCCCCAGCTGTCTCGCTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
 0376 AACATCTCCGCCCTCCGTGAGGAGACCTCCGAGCAGCTGGTGGCGTGAAGCCCTGGATCACTGCCAGAAC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
 0451 TCCCGGTGCTGGAGCTGAGTCAGTCAGCCGACTCCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

Flex←→hinge
 A T A P T A P E P K S C D K T H T C P P C P A P E
 0526 GCCACACCCCCGACAGCCCCGAGCCAAATCTGTGACAAAATCACACATCCCCACCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
 0601 CTCCCTGGGGGACCGTCAAGTCCTCTTCCCTCCAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
 0676 GTCACATGCGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTCAACTGGTACGGTACGGACGGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
 0751 GTGCATAATGCCAAGAACAGCCGGAGGAGCAGTACAACAGCACGTACCGGTGGTCTGCTCCCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
 0826 CTGCACCAAGGACTGGCTGAATGCCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
 K T I S K A K G Q P R E P Q V Y T L P P S R D E L
 0901 AAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCCAGGTGTACACCCCTGCCCTACCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
 0976 ACCAAGAACCAAGGTCAAGCTGCCCTGACCTGCCCTGGTCAAAGGCTCTATCCAGCGACATCGCGTGGAGGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
 1051 ATGGGAGCCGGAGAACAACTACAAGAACCCAGCCTCCGTGACTCCGACGGCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
 1126 AAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCATGTCCTGATGCATGAGGCTCTGCAC 1200

CH3←→VH
 N H Y T Q K S L S L S P G K Q V Q L V Q S G G G V
 1201 AACCAACTACACGCAGAACAGAGCCTCTCCCTGTCTCCCGTAAACAGGTGCAGCTGGTGCAGTCTGGCGTGGAGTG 1275

V Q P G R S L R L S C K A S G Y T F T S Y V M H W
 1276 GTCCAGCCCGCCGAGCCCTGAGGTGCTGCAAGGCATGGCTACACCTTCACAGCTACGTGATGACATGG 1350

V R Q A P G K G L E W I G Y I V P Y N D G T K Y N
 1351 GTGCGCCAAGCCCCGGAAAGGGCTCGAATGGATTGGCTACATTGTGCTTATAATGACGGTACTAAGTACAAT 1425

E K F K G R F T I S S D K S K S T A F L Q M D S L
 1426 GAAAAGTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAACTAACCGCATCCCTCAAATGGACAGCTTG 1500

R P E D T A V Y Y C A R G S R Y D W Y L D Y W G Q
 1501 CGTCCAGAGGACACCCCGTATACTATTGTGTGCGCCGAGCCGTTACGACTGGTACTGGACTACTGGCCAA 1575

VH←→Linker
 G T P V T V S S G G G G G G G G S G G G G S N I
 1576 GGCACCTCAGTCACCGCTCTCCCTGGCGGTGGAGGCTCTGGTGGAGGCGGTTCAAGGAGGCGGTGGATCTAACATC 1650

M M T Q S P S S L S A S V G D R V T I T C K S S Q
 1651 ATGATGACTCAGAGCCCATCCAGCTTGAGCGCATCAGTAGGCAGCCGTAACGATCACTTGCAAATCCTCTCAG 1725

S V L Y S S N Q K N Y L A W Y Q Q T P G K A P K L
 1726 TCAGTATTGTACTCCAGCAACCAGAACGAAACTACCTGGCCGGATATCAGCAGACTCCGGCAAAGCCCCAAAGTTG 1800

L I Y W A S T R E S G V P S R F S G S G S G T D Y
1801 CTGATTATTGGGCCCTCCACGCGCGAGTCTGGCGTGCATCACGCTTAGCGGCAGCGGGTCCGGTACAGATTAC 1875

T F T I S S L Q P E D I A T Y Y C H Q Y F S S Y T
1876 ACGTTTACCAATTAGCAGTCTGCAGCTGAGGACATAGCCACCTACTACTGTCAACAGTACTTTAGTTCCCTACACT 1950

V_L←|
F G Q G T K L Q I T R STOP
1951 TTTGGCCAGGGAACTAAACTGCAGATTACTCGATGA

1986

Figure 18B

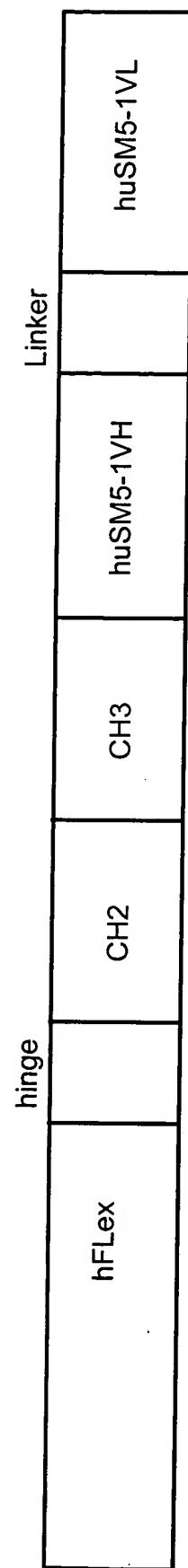


FIGURE 19

Figure 20A

→SP SP←→VH
M E W S W I F L F L L S G T A G V H S E V
0001 CTTGCCGCCACATGGAATGGAGTGGATATTCTCTTCCTGTCAGGAACGTGAGGCTTCAGTGAAGATGCTCTGCAAGGCTTCTGGATAC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGCTTCAGTGAAGATGCTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGTGAAGCAGAAGCCTGGCAGGCCCTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTCAAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGGGTCTATTATTGTCTACGGTAGTAGGTAC 0375
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTAGATGTCGGGGCGAGGACACGGTCACCGTCTCAGCTGACCAAGGGCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGACCCCTCTCAAGAGCACCTCTGGGGCACAGGGCCCTGGGTCTGGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTCTTGGAAACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCCTCAGCAGCTGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACACCAAGGTGACAAGAAAGTGGTGAAGAGGCCACACAGGGAGGGAGGGT 0750
0751 TCTGCTGGAAAGCAGGCTCAGGGCTCTGCCTGGACGCATCCCGCTATGCGAGCCCAGTCCAGGGCAGCAAGGA 0825
0826 GGCCCCGGTCTGCCCTCTCACCGGAGCCCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTCTGGCTTTTC 0900
0901 CCAGGGCTCTGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGCAGGTGCTGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGAGGGCCCTGCCCTGACCTAACGCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTCTCTCTCCAGATTCAGTAACCTCCATCTCTCTGCAGAGGCCAAACTCTGTGA 1125
K T H T C P P C P
1126 CAAAACATCACACATGCCACCGTGCCAGGTAAAGGCCAGCCAGGCCCTGCCCTCAGCTCAAGGGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCCTGCATCCAGGGACAGGCCAGGCCGGTGTGACACGTCACCCATCTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTCTCTCCCTCCCCAAAACCAAGGACACCCATGATCTCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGCTCGCTCC 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAAACAAGCCCTCCAGCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCAAAGCCAAGGTGGACCCGTGGTGGAGGGCCACATGGACAGAGGCCGCTCGG 1650
G Q P R E P Q V Y T
1651 CCACCCCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGCTCAAGGGCAGCCCGAGAACCAAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCTCCATCCGGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGACCTGGTCAAGGCTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGAGAGCAATGGCAGCGAGAACAACTACAAGAACCGCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CGACGGCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCACAGGGAAACGTCTTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCGGTGATGCAAGGGCTCTGCAACACCAACTACAAGCAAGAGGCCCTCCCGTGTCTCCGGTAAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCTTCCAACACAGCCCCATCTCCCTCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCCTCAACCTGCAGGACGAGGAGCTCGCGGGGCCCTGCGCGCTGGTCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P S C L R F V Q T N I S R
2251 AGATACACMTGTACCAAAATGTGCCTTCAGCCCCCCCCAGCTGCTTCGCTTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACCTCTCCGGTGCC 2400

E L O C O P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTCAAGCCGACTCCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 20B

Figure 21A

→SP SP←→VH
 M E W S W I F L F L L S G T A G V H S E V
 0001 CTTGCCGCCACCATGGAATGGAGTTGGATTTCTCTCTGTCAGGAACGTGAGGTGTCACCTCTGAGGTC 0075

Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
 0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGCTTCAGTAAGATGTCTGCAAGGCTCTGGATAC 0150

T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
 0151 ACATTCACTAGCTATGTTATGCACTGGTGAGCAGAGCCTGGGAGGGCTTGACTGGATTGGATATTTGTT 0225

P Y N D G T K Y N E K F K G K A T L T S D K S S S
 0226 CCTTACAATGATGGCACTAACATGAGAAGTTCAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGC 0300

T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
 0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGCTCTATTATTGTCTACGGTAGTTAC 0375

VH←→CH
 D W Y L D V W G A G T T V T V S S A S T K G P S V
 0376 GACTGGTATTAGATGTCGGGCCAGGGACCAAGGTCACCGTCTCCAGCTAGCAGCAAGGGCCATGGTC 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCCCTGGACCCCTCTCAAGGACACCTCTGGGGCAGCGCCCTGGCTGCCTGGTCAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGGTGCACACCTTCCGGCTGTCCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
 0676 AACGTGAATCACAAGCCACCAACCAAGGTGGACAAGAAAGTTGGAGAGGCCAGCAAGGGAGGGAGGGTG 0750

0751 TCTGCTGGAAAGCAGGCTCAGCGCTCTGCCTGGACGCATCCGGCTATGCAGCCCAGTCAGGGCAGCAAGGCA 0825

0826 GGCCCCGCTGCCCTCTCACCCGGACCTCTGCCGCCACTCATGGTCAGGGAGAGGTCTCTGGCTTTTC 0900

0901 CCAGGCTCTGGGAGGGCACAGGCTAGGTGCCCCCTAACCCAGGCCCTGCACACAAAGGGCAGGTGCTGGCTCAG 0975

0976 ACCTGCCAACAGGCCATATCGGGAGGACCCCTGCCCTGACCTAACCCACCCAAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
 1051 TCAGCTGGACACCTTCTCTCTCCAGATTCCAGTAACCTCCATCTCTCTGCAGGCCAACATCTGTGA 1125

K T H T C P P C P
 1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAGGCCAGGCCAGGCCCTCCAGCTCAAGGCCAGGGTG 1200

A P
 1201 CCCCTAGAGTAGGCTGCATCCAGGGACAGGCCAGGCCAGGCCCTGCTGACAGTCCACCTCCATCTCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAACTCTGGGGGACCGTCAGTCTCTCTCCCTCCAAAACCAAGGACACCCATGATCTCCGGACCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGGTACATCGTGGTGGTGACGTCAGGCCACGAAGACCTGAGGTCAAGTTCACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
 1426 TGGAGGTGCTAAATGCCAACAGACAAAGCCGGGAGGAGCAGTACAACAGCAGTCACCGGGTGGCTGCGTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CCGCCCTGCCACCAGGACTGGCTGAATGCCAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCA 1575

E K T I S K A K
 1576 TCGAGAAAACCATCTCAAAGCCAAGGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGCTCGGC 1650

G Q P R E P Q V Y T
 1651 CCACCCCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGGCCAGAACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCTGCCATCCGGATGAGCTGACCAAGAACAGGTGACCTGCCCTGCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATGCCGTGGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCAAGGCCCTCCGTGCTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCTCAT 1950

CH←→Linker
 S V M H E A L H N H Y T Q K S L S L S P G K G G G
 1951 GCTCCGTGATGCATGAGGCTCTGCACAAACCAACTACACCGCAGAAGAGCAGGCCCTCCCTGTCTCCGTAAAGGCCGTG 2025

Linker←→FLex

G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTCAAGGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100

D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTCAGATTACCCAGTCACCGTGGCCTCCAACC 2175

Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGCTCTGGCGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250

A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACTTGTCAACAAATGTGCCTTTC 2325

P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCCAGCTGCTTCGCTTCGCTCCAGACCAACATCTCCGCTCTGCAGGAGACCTCCGAGCAGCTGG 2400

A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACCTTCTCCGGTGCAGTGTCAAGCCCCACTCCTCAA 2475

L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 21B

Figure 22A

→SP
 M T V L A P A W S P T T Y L L L L L L L S S G L S
 0001 ATGACAGTGCTGGCCAGGCCCTGGAGCCAAACAACCTATCTCCCTCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLex
 G T Q D C S F Q H S P I S S D F A V K I R E L S D
 0076 GGGACCCAGGACTGCTCCCTCAACACAGCCCCATCTCCCTGGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G G L W R
 0151 TACCTGCTTCAGATTACCCAGTCACCGTGGCCCTCAACCTGCAAGGAGCTCTGCGGGGCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
 0226 CTGGTCCCTGGCACAGCGCTGGATGGAGCGCTCAAGACTGTCGCTGGTCAAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
 0301 GTGAAACACGGAGATACTTGTCAACCAATGTGCCCTTCAGCCCCCCCCAGCTGTCGCTTCGTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
 0376 AACATCTCCGCCCTCCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAAC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
 0451 TCCCGGTGCTGGAGCTGCAGTGTCAGCCGACTCCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

FLex←→hinge
 A T A P T A P E P K S C D K T H T C P P C P A P E
 0526 GCCACAGCCCCGACAGCCCCGGAGCCAAATCTGTGACAAAACACTACACATGCCACCGTGCCAGCAC 0600

L L G G P S V F L F P P P K P K D T L M I S R T P E
 0601 CTCCCTGGGGGACCGTCAGTCCTCTCCCTCCCTCAAAGGACACCCCTCATGATCTCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
 0676 GTCACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTTCACTGGTACGTGGACGGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
 0751 GTGCATAATGCCAAGAACAGCCGGAGGAGCAGTACAACAGCACGTACCGGGTGGCTGCGTCCCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
 0826 CTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
 K T I S K A K G Q P R E P Q V Y T L P P S R D E L
 0901 AAAACCATCTCCAAAGCAGGGCAGCCCCGAGAACCCACAGGTGACACCCCTGCCCTCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
 0976 ACCAAGAACCCAGGTCAACCTGACCTGGCTAAAGGTTCTATCCAGCGACATGCCGTGGAGTGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
 1051 AATGGGAGCCGGAGAACAACTACAAGAACCCACGCCCTCCGTGACTCCGACGGCTCTTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
 1126 AAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCTCTCATGCTCGTGTGATGAGGCTCTGCAC 1200

CH3←→VH
 N H Y T Q K S L S L S P G K E V Q L Q Q S G P E L
 1201 AACCAACTACACGCAGAACAGAGCTCTCCCTGTCTCCCGTAAAGAGGTCCAGCTGCACAGCTGGACCTGAGCTG 1275

V K P G A S V K M S C K A S G Y T F T S Y V M H W
 1276 GTAAAGCCTGGGCTTCAGTGAAGATGTCTGCAAGGCTCTGGATACACATTCACTAGCTATGTTATGCACTGG 1350

V K Q K P G Q G L D W I G Y I V P Y N D G T K Y N
 1351 GTGAAGCAGAACCTGGGAGGGCTTGACTGGATTGGATATATGTTCTTACAATGATGGCAACTAACAT 1425

E K F K G K A T L T S D K S S S T A Y M E L S R L
 1426 GAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACATGGAGCTCAGCAGACTG 1500

T S E D S A V Y Y C V Y G S R Y D W Y L D V W G A
 1501 ACCTCTGAGGACTCTCGGGCTATTATGTGCTACCGTAGGTACGACTGGTATTAGATGTCGGGGCGCA 1575

VH←→Linker
 G T T V T V S S G G G G S G G G G G G G G S N I
 1576 GGGACACGGTCACCGTCTCTCAGGGGGTGGAGGCTCTGGTGGAGGGCTCAGGAGGGCTGGATCTAACATT 1650

Linker←→V_L
 M M T Q S P S S L A V S A G E K V T M S C K S S Q
 1651 ATGATGACACAGTCGGCCATCATCTCTGGCTGTCTGCAAGGAGAAAAGGTCACTATGAGCTGTAAGTCCAGTC 1725

S V L Y S S N Q K N Y L A W Y Q Q K P G Q S P K L
1726 AGTGTGTTATACAGTCAAATCAGAAGAACTACTTGGCTGGTACAGCAGAAACAGGGCAGTCTCTAAACTG 1800

L I Y W A S T R E S G V P D R F T G S G S G T D F
1801 CTGATCTACTGGGCATCCACTAGGGAAATCTGGTGTCCCTGATCGCTCACAGGCAGTGGATCTGGGACAGATTTT 1875

T L T I S S V Q A E D L A V Y Y C H Q Y F S S Y T
1876 ACTCTTACCATCAGCAGTGTACAAGCTGAAGACCTGGCAGTTTATTACTGTCAATATTCCTCCTACACG 1950

$v_L \leftarrow |$

F G G G T K L E I K R stop
1951 TTGGAGGGGGGACCAACCTGGAAATAAGCGGTGA

1986

Figure 22B

Figure 23

→SP SP ← | →V_H
 M G F S R I F L F L L S V T T G V H S Q V Q L
 0001 GCCACCATGGGATTCAGCAGGATTTTCTCTCCCTGTCAGTAACTACAGGTGTCACTCCCAGGTAACTA 0075

Q Q P G A E L V K P G A S V K M S C K A S G Y T F
 0076 CAGCAGCCTGGGCTGAGGCTGGTGAAGCCTGGGCCTGTCAGGTAAGGTGTCTGCAGGCTGCTA 0150

T S Y N M H W V K Q T P G R G L E W I G A I Y P G
 0151 ACCAGTTAATTGCACTGGTAAGCAGACCCTGGTCGGGCTGGAAGGTGGGCTTATTATCCAGGA 0225

N G D T S Y N Q K F K G K A T L T A D K S S S T A
 0226 AATGGTGATCTCCTAATCAGAGGTCAAGGCCAGCCACTGACTGCAGACAAACTCCCCAGCAGCC 0300

Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
 0301 TACATGCAGTCAGCGGCTGACATCTGAAGACTTCGGGTCTATTACTTGTGCAAGTCGACTTACGGCGGT 0375

D W Y F N V W G A G T T V T V S A
 0376 GACTGGTACTTCAATGTCTGGGGGCAGGGCCACGGTCACCGTCTGCA 0426

Figure 24

→SP SP ← | →V_L
 M D F Q V Q I F S F L L I S A S V I M S R G Q I
 0001 ACCATGGATTTCAGATTTCAGTTCTCGTATCAGTGCTTCAAATGTCCAGGGACAATT 0075

V L S Q S P A I L S A S P G E K V T M T C R A S S
 0076 GTTCTCCCAGTCTCAGAATCCTGTCTGCATCTCAGGGGAAGGTCACAATGTCAGGGGCAGCTCA 0150

S V S Y I H W F Q Q K P G S S P K P W I Y A T S N
 0151 AGTGTAAGTTACTCCACTGTTCAGCAGAGGCAGGATCCTCCCCAACCCTGATTATGCCACATCCAAC 0225

L A S G V P V R F S G S G S G T S Y S L T I S R V
 0226 CTGGCTTTGGGATTCCCCTGTCGCTTCAGTGGCAGTGGGCTGGGACTTTACTTCTCACAATCAGTAAGTG 0300

E A E D A A T Y Y C Q Q W T S N P P T F G G G T K
 0301 GAGGCTGAGAGTGTCCCACTTTTACTGCCAGCGAGTGGGACTACCACCCAGTTCGGTGGGACAAG 0375

V_L ← |
 L E I K R
 0376 CTGGGAGATCAACGA 0390

Figure 25

↓SP SP ← | → V_H
 M G F S R I F L F L L S V T T G V H S Q V Q L
 0001 GCCACCATGGGATTCAAGCAGGATCTTCTCTCCCTGTCAGTAACACTACAGGTGTCCACTCCAGTACAACTA 0075
 Q Q P G A E L V K P G A S V K M S C K A S G Y T F
 0076 CAGCAGCCTGGGCTGAGCTGGTGAAGCCTGGGCTCACTGAAGATGTCTGCAAGGCTTCTGGTACACATT 0150
 T S Y N M H W V K Q T P G R G L E W I G A I Y P G
 0151 ACCAGTTACAATATGCACTGGTAAGCAGACACCTGGTGGGCTGGAATGGATTGGAGCTATTATCCAGGA 0225
 N G D T S Y N Q K F K G K A T L T A D K S S S T A
 0226 AATGGTGTACTTCTACAATCAGAAGTTCAAGGCAAGGCCACACTGACTGCAAGACAAATCTCCAGCACAGCC 0300
 Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
 0301 TACATGCAGCCTAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATGCACTTACAGGGGT 0375
 D W Y F N V W G A G T T V T V S A A S T K G P S V
 0376 GACTGGTACTTCAATGTCTGGGCGCAGGGACACGGTCAAGGCTGGTC 0450
 F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCCCTGGCACCCCTCCAAAGAGCACCTCTGGGACAGCGCCCTGGGCTGGTCAGGACTACAGGGGT 0525
 P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACGGTGACGGTCTTGGAAACTCAGGCGCCCTGACCAGCGCGTGCACCCCTCCGGCTGTCACAG 0600
 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTGGGACCCAGACCTACATCTGC 0675
 N V N H K P S N T K V D K K V
 0676 AACGTGAATCACAAGCCCAGCAACACCAAGGTGACAAGAAAGTGGTAGAGAGGCCAGCACAGGGAGGGAGGGT 0750
 0751 TCTGGTGAAGCAGGCTCAGGCTCTGGACGCTCCGGCTATCCGGCTATCGAGCCCCAGTCAGGGCAGCAAGGCA 0825
 0826 GGCCCCGGTCTGCCCTCTGGGAGCCCTGCCCCACTCATGCTCAGGGAGAGGGTCTCTGGCTTTTC 0900
 0901 CCAGGCTCTGGGAGGCACAGGCTAGGTGCCCCCTAACCCAGGCCCTGACACAAAGGGCAGGTGCTGGCTCAG 0975
 0976 ACCTGCCAAGAGCCATATCCGGAGGACCTGGCCCTGACCTAACCCACCCCAAGGCCAAACTCTCCACTCCC 1050
 1051 TCAGGCTGGACACCTCTCTCTCCAGATTCCAGTAACTCCCAATCTCTCTGCAAGGCCAAACTCTTGTA 1125
 K T H T C P P C P
 1126 CAAAACACATGCCACCGTGCCAGGTAAAGCCAGGCCAGGGCTCGCCCTCAGCTCAAGGCCAGGGACAGGTG 1200
 A P
 1201 CCCTAGAGTAGCCCTGCATCCAGGGACAGGCCAGGCCGGTGTGACACGTCCACCTCCATCTCTCTCAGCAC 1275
 E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAACTCTGGGGACCGTCAGTCTTCCCTCTCCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCC 1350
 E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGGTACATGGCTGGTGGACGTGAGCCACGAAGACCTGAGGTCAACTGTACTGGTACGTGGACGGGG 1425
 E V H N A K T K P R E E Q Y N S T Y R V V S V L T
 1426 TGGAGGTGATAATGCCAAGACAAAGCCGGAGGAGCAGTACAACAGCACCTACCGGGTGGCTGGCTCTCA 1500
 V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CCGTCTGCACCAGGACTGGCTGAATGCCAAGGAGTACAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCCA 1575
 E K T I S K A K
 1576 TCGAGAAAACCATCTCAAAGCCAAGGTGGGACCCCTGGGGTGCAGGGCCACATGGACAGAGGCCGGCTGGC 1650
 G Q P R E P Q V Y T
 1651 CCACCCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGCTCACAGGGCACCCCGAGAACCAAGGTGACA 1725
 L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCTCATCCGGATGAGCTGACCAAGAACCGGTCAAGCTGGCTGACCTGGTCAAAGGCTTCTATCCC 1800
 D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGCAGCGAGAACACTACAAGACCCAGCCTCCGGTGTGGACT 1875
 D G S F F P L Y S K L T V D K S R W Q O G N V F S C
 1876 CCGACGGCTCTTCTCCCTACAGCAAGCTCACCGTGGACAGAGCACGGTGGCAGCAGGGAACGGTCTCTCA 1950
 S V M H E A L H N H Y T Q K S L S L S P G K STOP
 1951 GCTCCGTATGCAAGGGCTCTGCAACACACTACAGCAGAGGAGCTCTCCCTGTCAGGGTAAATGA 2021

Figure 26

→SP SP ← | → VL
M D F Q V Q I F S F L L I S A S V I M S R G Q I
0001 ACCATGGATTTCAAGTCAGATTTCAAGCTCAGCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAATT 0075

V L S Q S P A I L S A S P G E K V T M T C R A S S
0076 GTTCTCTCCAGTCTCCAGCAATCCCTGCTGATCTCCAGGGAGAAGGTCAACATGACTTGCAGGGCAGCTCA 0150

S V S Y I H W F Q Q K P G S S P K P W I Y A T S N
0151 AGTGTAAAGTTACATCCACTGGTCCAGCAGAAGCCAGGATCCTCCCCAAACCCCTGGATTATGCCACATCCAAC 0225

L A S G V P V R F S G S G S G T S Y S L T I S R V
0226 CTGGCTCTGGAGTCCCTGTCGCTTCAGTGGCAGTGGCTGGGACCTCTACTCTCTACAATCAGTAGAGTG 0300

E A E D A A T Y Y C Q Q W T S N P P T F G G G T K
0301 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCGTGGTGGACCAAG 0375

VL ← | → CL
L E I K R T V A A P S V F I F P P S D E Q L K S G
0376 CTGGAGATCAAACGAACCTGGCTGCACCATCTGCTCTCATCTCCGCCATCTGATGAGCAGTTGAAATCTGGA 0450

T A S V V C L L N N F Y P R E A K V Q W K V D N A
0451 ACTGCCTCTGTTGTGCTGCTGATAACTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCC 0525

L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0526 CTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGCAGCACCTACAGCCTCAGCAGCACC 0600

L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0601 CTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCTGAGCTCG 0675

P V T K S F N R G E C Stop
0676 CCCGTACAAAGAGCTCAACAGGGAGAGTGTTAG 0711

Figure 27A

0001 GCCACCATGGGATTCAAGCAGGATCTTCTCTCCCTGCAAGTAACACTACAGGTGTCCACTCCAGGTACAAC 0075

0076 Q Q P G A E L V K P G A S V K M S C K A S G Y T F
CAGCAGCCTGGGCTGAGCTGGTGAAGCCTGGGCTCAGTGAAGATGCTCTGCAAGGCTCTGGTACACATT 0150

0151 T S Y N M H W V K Q T P G R G L E W I G A I Y P G
ACCAGTTACAATATGCACGGTAAAGCAGACACCTGGTGGGCTGGAATGGATTGGAGCTATTATCCAGGA 0225

0226 N G D T S Y N Q K F K G K A T L T A D K S S S T A
AATGGTGTATACTCCTACAATCAGAAGTTCAAGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCC 0300

0301 Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
TACATGCAGCCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTTACTGTCAAGGATCGACTTACACGGCGGT 0375

0376 D W Y F N V W G A G T T V T V S A A S T K G P S V
GACTGGTACTTCATGTCTGGGGCGCAGGGACACGGTCAAGGCTCTGGTCAAGGACTACTTC 0450

0451 F P L A P S S K S T S G G T A A L G C L V K D Y F
TTCCCCCTGGCACCCCTCCAAAGAGCACCTCTGGGGCACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525

0526 P E P V T V S W N S G A L T S G V H T F P A V L Q
CCCGAACGGTGACGGTCTTGAAGACTCAGGCCCTGACCAGGGCGTGCACACCTTCCGGCTGCTACAG 0600

0601 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
TCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTGGGACCCAGACTACATCTGC 0675

0676 N V N H K P S N T K V D K K V
AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGGAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGCTGGAAGCAGGCTCAGGCCCTCCCTGGACGCATCCCGCTATGCGAGCCCCAGTCAGGGCAGCAAGGCA 0825

0826 GGCCCCGCTCGCTCTTCAACCCGGAGCCTCTGCCGCCCCACTCATGCTCAGGGAGAGGGTCTCTGGCTTTTC 0900

0901 CCAGGCTCTGGCAGGGACAGGCTAGGTGGCCCTAACCCAGGCCCTGCACACAAAGGGGAGGTCTGGCTCAG 0975

0976 ACCTGCCAAGGCCATATCCGGAGGGACCCCTGCCCTGACCTAACGCCACCCAAAGGCCAAACTCTCCACTCCC 1050

1051 E P K S C D
TCAGGCTGGACACCTCTCTCCCTCCCAGATTCCAGTAACTCCCAATCTCTCTGCAAGGCCAAACTCTGTGA 1125

1126 K T H T C P P C P
CAAAACTCACACATGCCACCGTGCCAGGTAAGGCCAGCCAGGCCCTCGCCCTCAGCTCAAGGCCAGGTG 1200

1201 A P
CCCTAAGTGTAGCTGCATCCAGGGACAGGCCCTGGCTGACACGTCCACCTCCATCTCTCTGCAAGGCCAC 1275

1276 E L L G G P S V F L F P P K P K D T L M I S R T P
CTGAACCTCTGGGGGACCGTCAAGTCTCTCTCCCTCAAGGACACCCCTCATGATCTCCGGACCC 1350

1351 E V T C V V V D V S H E P E V K F N W Y V D D G V
CTGAGGTACATGGCTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCG 1425

1426 E V H N A K T K P R E E Q Y N S T Y R V V S V L T
TGGAGGTGCAATGCCAACAGACAAAGCCGGGAGGGACAGTACAACAGCACGTACCGGGTGGCTCGCTC 1500

1501 V L H Q D W L N G K E Y K C K V S N K A L P A P I
CCGTCCTGCACCAGGACTGGCTGAATGCCAACAGGTGGACCCCTGGTGGCGAGGGCCACATGGACAGAGGCCGGCTGGC 1575

1576 E K T I S K A K
TCGAGAAAACCATCTCCAAAGCCAAAGGTGGACCCCTGGTGGCGAGGGCCACATGGACAGAGGCCGGCTGGC 1650

1651 G Q P R E P Q V Y T
CCACCCCTGCCCCCTGAGAGTGAACCGCTGTACCAACCTCTGCTACAGGGCAGCCCCGAGAACCAAGGTGTACA 1725

1726 L P P S R D E L T K N Q V S L T C L V K G F Y P S
CCCTGCCCTCCATCCGGATGAGCTGACCAAGAACAGGTCAAGCTGACCTGGCTCAAAGGCTCTATCCCA 1800

1801 D I A V E W E S N G Q P E N N Y K T T P P V L D S
GCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGAACCCACGCGCTCCGGTGTGGACT 1875

1876 D G S F F L Y S K L T V D K S R W Q Q G N V F S C
CCGAGGGCTCTTCTTACAGCAAGGCTACCGTGGCAAGAGCAGGTGGCAGCAGGGGAGAACGGTCTCTCAT 1950

CH \leftarrow →FLEX

S V M H E A L H N H Y T Q K S L S L S P G K T Q D
 1951 GCTCCGTATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCCTCCCTGTCTCCGGTAAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
 2026 ACTGCTCCTCCAACACAGCCCCATCTCCCTCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
 2101 AAGATTACCCAGTCACCGTGGCCTCAACCTGCAGGACGAGGAGCTCTGCAGGGGGCCTCTGGCGGCTGGTCCGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
 2176 CACAGCCCTGGATGGACCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
 2251 AGATACACTTGTCAACAAATGTGCCTTCAGCCCCCCCCAGCTGTCCTCGCTCGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
 2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACCTCTCCGGTGC 2400

E L Q C Q P D S S T L P P P W S P R P L E A T A P
 2401 TGGAGCTGCAGTGTCAAGCCCCACTCCTCAACCTGCCACCCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
 2476 CGACAGCCCCGTGA 2489

Figure 27B

Figure 28A

0001 GCCACCATGGGATTCAAGCAGGATCTTCTCTCCCTGTCAGTAACACTACAGGTGTCCACTCCACAGTACAACATA 0075

0076 Q Q P G A E L V K P G A S V K M S C K A S G Y T F
CAGCAGCCTGGGCTGAGCTGGTGAAGCCTGGGCTCAGTGAAGATGTCTGCAAGGCTCTGGCTACACATT 0150

0151 T S Y N M H W V K Q T P G R G L E W I G A I Y P G
ACCAGTTACAATATGCACGGTAAAGCAGACACCTGGTCAGGCTGGATGGAGCTATTATCCAGGA 0225

0226 N G D T S Y N Q K F K G K A T L T A D K S S S T A
AATGGTGTATACTCTACAATCAGAAGTTCAAGGCCACACTGACTGCAGACAAATCTCCAGCACAGCC 0300

0301 Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
TACATGCAGCCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGAGTCAGTACTACGGCGGT 0375

0376 D W Y F N V W G A G T T V T V S A A S T K G P S V
GACTGGTACTTCATGTCTGGGGCGCAGGGACCAAGGTCTGCGGTCTCTGAGCTAGCACCAAGGGCCATCGTC 0450

0451 F P L A P S S K S T S G G T A A L G C L V K D Y F
TTCCCCCTGGCACCCCTCCAAGAGCACCTCTGGGGCACAGGGCCCTGGGTCTGGCTAGCACCAAGGGCCATCGTC 0525

0526 P E P V T V S W N S G A L T S G V H T F P A V L Q
CCCGAACCGGTGACGGTGTCTGGAACTCAGGCCCTGACCAGCGCGTGCACACCTCCGGCTGTCTACAG 0600

0601 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
TCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTGC 0675

0676 N V N H K P S N T K V D K K V
AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTGTGGAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGTGGAAGCAGGCTCAGGCCCTCTGGACGATCCGGCTATGAGCAGCCCAGTCCAGCAGGGCTGTGCAAGGCA 0825

0826 GGCCCGTCTGGCTCTCACCCGGAGCCTCTGGCCGCCACTCATGCTCAGGGAGAGGGCTCTGGCTTTTC 0900

0901 CCAGGCTCTGGCAGGCACAGGCTAGGTGCCCCCTAACCCAGGCCCTGACACAAAGGGCAGGTGTGGCTCAAG 0975

0976 ACCTGCAAGAGCCATATCGGGAGGACCCCTGACCTAACGCCACCCCAAGGCCAAACTCTCCACTCCC 1050

1051 E P K S C D
TCAGCTGGACACCTCTCTCTCCAGATTCCAGTAACCTCCAAATCTCTCTGCAAGGCCAAACTCTTGTA 1125

1126 K T H T C P P C P
CAAACATCACACATGCCACCGTCCCCAGGTAAAGCCAGGCCAGGCCCTGCCCTCCAGCTCAAGGGGGACAGGTG 1200

1201 A P
CCCTAGAGTAGGCTGCATCCAGGGACAGGCCAGGCCAGGCCGGTGTGACACGTCCACCTCCATCTCTGGCTCAGCAC 1275

1276 E L L G G P S V F L F P P K P K D T L M I S R T P
CTGAACCTCTGGGGGACCGTCAGTCTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCC 1350

1351 E V T C V V V D V S H E P E V K F N W Y V D D G V
CTGAGGTACATGCCAGGTGGACGGCAGGCCAGGCCGGTGTGACACGTCCACCTCCATCTCTGGACGGGG 1425

1426 E V H N A K T K P R E E Q Y N S T Y R V V S V L T
TGGAGGTGATAATGCCAGAACAGGCCAGGCCAGGCCGGTGTGACACGTACACAGCACGTACGGGTGGCTGCGTCTCA 1500

1501 V L H Q D W L N G K E Y K C K V S N S K A L P A P I
CCGTCCTGCACCAAGGACTGGCTGAATGCCAGGACTCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCA 1575

1576 E K T I S K A K
TCGAGAAAACCATCTCAAAGCCAAAGGTGGACCCCTGGGTGCGAGGGCACATGGACAGAGGGCCGCTCGGC 1650

1651 G Q P R E P Q V Y T
CCACCCCTCTGCCCTGAGAGTACCCGCTGTACCAACCTCTGTCACAGGGCAGGCCAGAACACAGGTGTACA 1725

1726 L P P S R D E L T K N Q V S L T C L V K G F Y P S
CCCTGCCCTCATCCCGGATGAGCTGACCAAGAACAGGTCAAGGTCTGACCTGCTGGTCAAAGGCTCTATCCCA 1800

1801 D I A V E W E S N G Q P E N N Y K T T P P V L D S
GCGACATCGCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGAACACGCCCTCCGGTCTGGACT 1875

1876 D G S F F L Y S K L T V D K S R W Q Q G N V F S C
CCGACGGCTCTCTCTACAGCAAGCTACCCGTTGACAAGAGCAGGTGGCAGCAGGGAAAGTCTCTCAT 1950

1951 S V M H E A L H N H Y T Q K S L S L S P G K G G G
GCTCCGTGATGCATGAGGCTCTGCAACACACTACACGCAAGAGGCCCTCTCCCTGTCCTCCGGTAAAGGGCTGG 2025

Linker←→FLex

G S G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTCAAGGAGGCGGTGGATCTACCCAGGACTGCTCCCTCCAACACAGCCCCATCTCCT 2100

D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAAATCCGTGAGCTGCTGACTACCTGCTTCAGATTACCCAGTCACCGTGGCCTCCAACC 2175

Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCGCGGGGCTCTGCGGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250

A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGTCCAAGATGCAAGCTTGCTGGAGCGCGTGAAACACGGAGATACTTTGTCACCAAATGTGCCCTTC 2325

P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCCAGCTGCTTCGCTTCAGACCAACATCTCCGCCCTGCAGGAGACCTCCGAGCAGCTGG 2400

A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACACTTCTCCGGTGCCTGGAGCTGCAGTGTCAAGCCGACTCCTCAA 2475

L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 28B

Figure 29A

→SP
 M T V L A P A W S P T T Y L L L L L L L S S G L S
 0001 ATGACAGTGCCTGGCGGAGCCCTGGAGCCAAACACTATCTCCCTCTGCTGCTGAGCTCGGGACTCACT 0075

SP←→Flex
 G T Q D C S F Q H S P I S S D F A V K I R E L S D
 0076 GGGACCCAGGACTGCTCCCTCAACACAGCCCCATCTCCCTGGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
 0151 TACCTGCTTCAGATTACCCAGTACCGTGGCCCTCAACCTGCAGGACGAGGAGCTCTGGGGCCCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
 0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGCTCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
 0301 GTGAAACACGGAGATACACTTGTGACCAAAATGTGCTTCAGCCCCCCCCAGCTGTCTCGCTTCGCTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
 0376 AACATCTCCGCTCTGCAAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
 0451 TCCCAGGTGCTGGAGCTGCAGTGTGAGCCGACTCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
 A T A P T A P E P K S C D K T H T C P P C P A P E
 0526 GCCACAGCCCCGACAGCCCCGGAGCCAAATCTTGACAAAATCACACATGCCACCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
 0601 CTCCCTGGGGGACCGTAGTCTCTCTTCCCCAAAACCCAGGACACCCCTCATGATCTCCGGACCCCTGAG 0675

V T C V V V W D V S H E D P E V K F N W Y V D G V E
 0676 GTCACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
 0751 GTGCATAATGCAAGAACAAAGCCGGGGAGGAGCAGTACAACAGCAGTACCCGGTGGCTCGCTCCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
 0826 CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
 K T I S K A K G Q P R E P Q V Y T L P P S R D E L
 0901 AAAACCATCTCAAACCCAAAGGGCAGCCCCGAGAACCCACAGGTGACACCCCTGCCCATCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
 0976 ACCAAGAACCCAGGTGACCTGACCTGGTCAAAGGCTTCTATCCAGCGACATGCCGTGGAGTGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
 1051 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGTGACTCCAGCGCTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
 1126 AAGCTACCCGTGGACAAGAGCAGGGTGGCAGCAGGGGAACGTCTCTCATGCTCCGTGATGCACTGAGGCTCTGCAC 1200

CH3←→VH
 N H Y T Q K S L S L S P G K Q V Q L Q Q P G A E L
 1201 AACCAACTACCGCAGAAGAGCCTCTCCCTGTCTCCCGTAAACAGGTACAACACTACAGCAGCTGGGCTGAGCTG 1275

V K P G A S V K M S C K A S G Y T F T S Y N M H W
 1276 GTGAAGCCTGGGGCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTTACAGTTACAATATGCAC 1350

V K Q T P G R G L E W I G A I Y P G N G D T S Y N
 1351 GTAAACAGACACCTGCTGGGGCTGGAATGATTGGAGCTTATCCAGGAAATGGTATACTTCCAC 1425

Q K F K G K A T L T A D K S S S T A Y M Q L S S L
 1426 CAGAAGTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTG 1500

T S E D S A V Y Y C A R S T Y Y G G D W Y F N V W
 1501 ACATCTGAAGACTCTGGCTATTACTGTGCAAGATGCACTTACAGGGGTGACTGGTACTTCATGTCTGG 1575

V_H ←→ Linker Linker←→
 G A G T T V T V S A G G G G S G G G G S G G G S
 1576 GGCAGGGACCACGGTCACCGTCTGCAAGGGTGGAGGCGGTTCAAGGAGGGTGGATCT 1650

→V_L
 Q I V L S Q S P A I L S A S P G E K V T M T C R A
 1651 CAAATTGTTCTCTCCAGTCTCCAGCAATCCTGTGATCTCCAGGGAGAAGGTACAATGACTTGCAAGGGCC 1725

S S S V S Y I H W F Q Q K P G S S P K P W I Y A T
1726 AGCTCAAGTGTAAAGTTACATCCACTGGTCCAGCAGAAGCCAGGATCCTCCCCAAACCTGGATTTATGCCACA 1800

S N L A S G V P V R F S G S G S G T S Y S L T I S
1801 TCCAACCTGGCTTCTGGAGTCCCTGTCGCTTCAGTGGCAGTGGCTCTGGACCTCTTACTCTCACAAATCACT 1875

R V E A E D A A T Y Y C Q Q W T S N P P T F G G G
1876 AGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTGGTGGGG 1950
V_b ← |

T K L E I K R STOP
1951 ACCAAGCTGGAGATCAAACGATGA

1974

Figure 29B

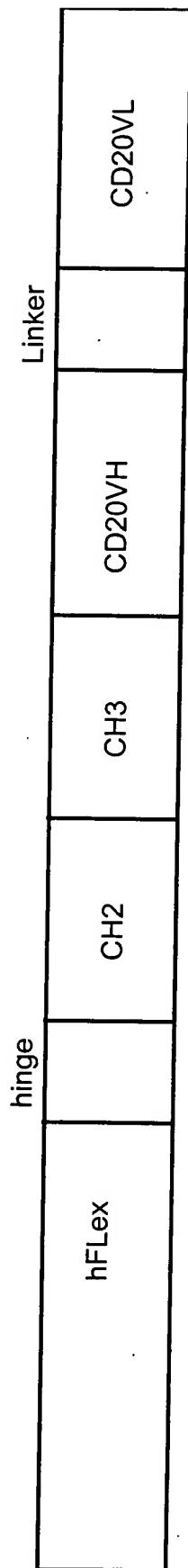


FIGURE 30

Figure 31

→SP SP←|→VH
 0001 M D F Q V Q I F S F L L I S A S V I I S R G E V Q ATGGATTTCAAGGTGAGATTTCAAGCTCCTGCTAATCAGTCAGTCATAATCCAGAGGAGGGTTCAAG 0075
 0076 L V E S G G G L V Q P G G S L R L S C A A S G F N CTGGTGGAGTCTGGCGGTGGCTGGTGCAGGCCAGGGGCTCACTCCGTTGTCCTGTCAGCTTCTGGCTTCAC 0150
 0151 I K D T Y I H W V R Q A P G K G L E W V A R I Y P ATTAAAGACACCTATATACACTGGTGCCTGAGGCCGGTAAGGGCTGGAATGGGTTGCAAGGATTATCCT 0225
 0226 T N G Y T R Y A D S V K G R F T I S A D T S K N T ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCGTTCACTATAAGCGCACACATCCAAAAACACA 0300
 0301 A Y L Q M N S L R A E D T A V Y Y C S R W G G D G GCCTACCTGCAGATGAACAGCCTGCGTGCAGGACACTGCCGTCTATTATTGTTCTAGATGGGAGGGACGGC 0375
 0376 F Y A M D Y W G Q G T L V T V S S TTCTATGCTATGGACTACTGGGTCAAGGAACCCCTGGTCACCGTCTCCTCG VH←| 0426

Figure 32

→SP SP←|→V_L
 0001 M D F Q V Q I F S F L L I S A S V I I S R G D I Q ATGGATTTCAAGGTGAGATTTCAAGCTCCTGCTAATCAGTCAGTCATAATCCAGAGGAGACATCCAG 0075
 0076 M T Q S P S S L S A S V G D R V T I T C R A S Q D ATGACCCAGTCCCCGAGCTCCCTGTCGGCTCTGTGGCGATAGGGTACCATCACCTGCCGTGCCAGTCAGGAT 0150
 0151 V N T A V A W Y Q Q K P G K A P K L L I Y S A S F GTGAATACTGCTGTAGCCTGGTATCAACAGAAACCCAGGAAAGCTCGAAACTACTGATTACTCGGCATCCTTC 0225
 0226 L Y S G V P S R F S G S R S G T D F T L T I S S L CTCTACTCTGGAGTCCCTCTCGCTCTGGCTCCAGATCTGGACGGATTCACTCGACCATCAGCAGTC 0300
 0301 Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K CAGCCGGAAGACTTCGCAACTTATTACTGTCAGCAACATTACTACTCCTCCACGTTGGACAGGGTACCAAG 0375
 0376 V E I K R GTGGAGATCAAACGT V_L←| 0390

Figure 33

↑SP SP←↑VH

0001 ATGGATTTCAGGTGCAGATTTCAGCTCCTGCTAACAGTGCCTCAGTCATAATATCCAGAGGAGAGGTTAG 0075

0076 CTGGTGGAGTCTGGCGGTGGCTGGTGCAGCCAGGGGCTACTCCGTTGTCTGAGCTCTGGCTTCAAC 0150

0151 ATTAAAGACACCTATATACACTGGTGCCTCAGGCCCGGTAAGGGCTGGAATGGTTGCAAGGATTATCCT 0225

0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGCCGTTCACTATAAGCGCAGACACATCCAAAACACA 0300

0301 GCCTACCTGCAGATGAA CAGCCTGCCTGCTGAGGACACTGCGCTATTATTGTTCTAGATGGGAGGGACGGC 0375

VH←↑CH

0376 TTCTATGCTATGGACTACTGGGTCAGGAACCCCTGGTCACCGTCTCCCGCTAGCACCAAGGGCCATGGTC 0450

0451 TTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGGTCAGGACTACTTC 0525

0526 CCCGAACCGGTGACGGTGCTTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTCCGGCTGCTACAG 0600

0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTGGCACCCAGACCTACATCTGC 0675

0676 AACGTGAATCACAGCCAGCAACCAAGGTGACAAGAAAGTTGGTAGAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGGCTGGACGCATCCCGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825

0826 GGCCCCGCTGCTCCCTTCAACCGGAGGCCCTGCCCCCCCACATGCTCAGGGAGAGGGCTTCTGGCTTTTC 0900

0901 CCAGGCTCTGGCAGGCACAGGCTAGGTGCCCCTAACCCAGGCCCTGACACAAAGGGCAGGTGCTGGCTCAG 0975

0976 ACCTGCCAAGAGCCATATCCGGAGGACCTGCCCCCTGACCTAAGCCACCCAAAGGCCAACTCTCCACTCCC 1050

1051 TCAGCTCGGACACCTTCTCTCCCTCCAGATTCCAGTAACCTCCAAATCTCTCTGAGCCAAATCTTGTA 1125

1126 CAAACTCACATGCCACCGTGCCCAAGGTAAAGCCAGGCCAGCCCTGCCCTCCAGCTCAAGGCCGGACAGGTG 1200

1201 CCCTAGAGTAGGCCTGCATTCAGGGACAGGCCCCAGCCGGTGCTGACAGTCCACCTCCATCTCTCCAGCAC 1275

1276 CTGAACTCCTGGGGGACCGTCAGTCTCTCTTCCCTCCACCCAAAGGACACCCCTCATGATCTCCGGACCC 1350

1351 CTGAGGTACATCGCTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTCACTGGTACGTGGACGGCG 1425

1426 TGGAGGTGCTATGCCAAGACAAGCCGGGAGGAGCAGTACAACAGCACGTCACGGTACCCGGTGGCTGCGTCTCA 1500

1501 CCGTCCTGCAACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGCTCCAAACAAAGCCCTCCAGCCCCA 1575

1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCACATGGACAGGGCCGCTCGGC 1650

1651 CCACCCCTGCCCCCTGAGAGTGACCGCTGTACCAACCTCTGCTACAGGGCAGCCCCAGAACACAGGTGACA 1725

1726 CCCTGCCCCCATCCGGATGAGCTGACCAAGAACAGGTGACCTGCTGGTCAAAGGCTTATCCCA 1800

1801 GCGACATGCCGTGGAGGGAGGCAATGGCAGCCGGAGAACACTACAAGACCCCTCCCGTGGACT 1875

1876 CCGACGGCTCTTCTTCCCTACAGCAAGGCTACCCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCTTCAT 1950

1951 GCTCCGTATGATGAGGCTCTGCACACCAACTACACCGAGAACAGGCTCTCCGTCTCCCGTAAATGA 2021

Figure 34

↑→SP SP←→V_L

M D F Q V Q I F S F L L I S A S V I I S R G D I Q
0001 ATGGATTTCAAGTGAGATTTCAAGCTTCTGCTAATCAGTCAGTCATAATATCAGAGGAGACATCCAG 0075

M T Q S P S S L S A S V G D R V T I T C R A S Q D
0076 ATGACCCAGTCCCCGAGCTCCCTGTCGCCCTCTGTGGCGATAGGGTACCATCACCTGCCGTGCCAGTCAGGAT 0150

V N T A V A W Y Q Q K P G K A P K L L I Y S A S F
0151 GTGAATACTGCTGTAGCCTGGTATCAACAGAAACCCAGGAAAAGCTCCGAAACTACTGATTCTACCGGCATCCCTTC 0225

L Y S G V P S R F S G S R S G T D F T L T I S S L
0226 CTCTACTCTGGAGTCCCTCTCGCTCTGGCTCCAGATCTGGACGGATTCACTCTGACCATCAGCAGTCG 0300

Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K
0301 CAGCCGGAAGACTTCGAACTTATTACTGTCAAGAACATTAACTACTCCTCCACGTTGGACAGGGTACCAAG 0375

V E I K R T V A A P S V F I F P P S D E Q L K S G
0376 GTGGAGATCAAACGTAATGCTGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGA 0450

T A S V V C L L N N F Y P R E A K V Q W K V D N A
0451 ACTGCCTCTGTTGTGCTGCTGAAATAACTCTATCCAGAGGCAAAGTACAGTGGAAAGGTGGATAACGCC 0525

L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0526 CTCCAATCGGTAACCTCCAGGAGACTGTCACAGAGCAGCACGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0600

L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0601 CTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCTGAGCTCG 0675

P V T K S F N R G E C Stop
0676 CCCGTCACAAAGAGCTCAACAGGGAGAGTGTAG 0711

Figure 35A

↑SP SP←→VH
 0001 M D F Q V Q I F S F L L I S A S V I I S R G E V Q ATGGATTTCAGGTGAGATTTCACTGCTCTGCTAACTCAGTCAGTCATAATCCAGAGGAGAGGTTCAAG 0075

L V E S G G G L V Q P G G S L R L S C A A S G F N CTGGTGGAGTCTGGCGGTGGCTGGTCAAGGCCAGGGGCTCACTCCGTTGTGCTGTGAGCTTCAGGCTTCAC 0150

I K D T Y I H W V R Q A P G K G L E W V A R I Y P ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGTAAGGGCTGGAATGGGTTGCAAGGATTATCCT 0225

T N G Y T R Y A D S V K G R F T I S A D T S K N T ACGAATGGTTATACTAGATATGCCGATAGCGTCAGGCCGTTCACTATAAGCGCAGACACATCCAAAAACACA 0300

A Y L Q M N S L R A E D T A V Y Y C S R W G G D G GCCTACCTGAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATGTTCTAGATGGGGAGGGACGGC 0375

VH←→CH
 0376 F Y A M D Y W G Q G T L V T V S S A S T K G P S V TTCTATGCTATGGACTACTGGGTCAAGGAACCCCTGGTCACCGTCTCCCTCGGCTAGCACCAAGGGCCATCGGTC 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F TTCCCCCTGGCACCCCTCCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGGCTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q CCCGAACCGGTGACGGTCTTGGAACTCAGGCGCCCTGACCAGGGCGTGCACACCTTCCGGCTGCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C TCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTCCAGCAGCTTGGGACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V AACGTGAATCACAAGCCAGCAACACCAAGGTGACAAGAAAGTTGGTGAAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGCTGGAAAGCAGGCTCAGCGCTCCTGGCTGGACGCATCCGGCTATGCCGCCCAGTCAGGGCAGCAAGGCA 0825

0826 GGCCCGTCTGCCCTTCACCCGGAGCCTCTGCCGCCACTCATGTCAGGGAGAGGTCTTCTGGCTTTTC 0900

0901 CCAGGCTCTGGGAGGCACAGGTAGGTGCCCCCTAACCCAGGCCCTGCACACAAGGGCAGGTGCTGGCTCAG 0975

0976 ACCTGCCAACAGGCCATATCGGGAGGACCTGCCCTGACCTAACGCCACCCAAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
 1051 TCAGCTCGGACACCTCTCTCCCTCCAGATTCCAGTAACCTCAATCTCTCTGCAAGGCCAAATCTGTGA 1125

K T H T C P P C P
 1126 CAAACTCACACATGCCACCGTGCCCGAGGTAAAGCCAGGCCAGGCCTGCCCTCCAGCTCAAGGCCGGACAGGTG 1200

A P
 1201 CCCTAGAGTAGCCCTGCATCCAGGGACAGGCCAGGCCAGGGTGCTGACAGTCACCTCCATCTCTCCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P CTGAACTCTGGGGGACCGTCAGTCTCTCTTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V CTGAGGTACATCGCTGGTGGTGGACGTGAGGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T TGGAGGTACATGCCAACAGGCCGGAGGAGCAGTACAACAGCACGTACCCGGTGGCTGGCTCCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I CCGCTCTGCCACAGGACTGGCTGAATGCCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCCA 1575

E K T I S K A K TCGAGAAACCATCTCCAAAGGCCAAAGGTGGGACCCGTGGGGTGCAGGGCACATGGACAGAGGCCGGCTCGGC 1650

G Q P R E P Q V Y T
 1651 CCACCCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCGAGAACACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCATCCGGATGAGCTGACCAAGAACAGGTCAAGCTGACCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E E N N Y K T T P P V L D S
 1801 GCGACATCGCCGTGGAGGTGGAGAGCAATGGCAGGCCAGAACACTACAAGACCCACGCCCTCCCGTGTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCCCTCTCTACAGCAAGGCTACCGTGGACAAGAGCAGGGCAGGCCAGGGACCGTCTCTCAT 1950

1951 S V M H E A L H N H Y T Q K S L S L S P G K T Q D
GCTCCGTATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAAACCCAGG 2025

CH \leftrightarrow FLex

2026 C S F Q H S P I S S D F A V K I R E L S D Y L L Q
ACTGCTCCTTCCAACACAGCCCCATCTCTCCGACTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

2101 D Y P V T V A S N L Q D E E L C G G L W R L V L A
AAGATTACCCAGTCACCGTGGCCTCCAACCTGCGAGGAGGAGCTGCGGGGCCCTCGCGCCTGTCCTGG 2175

2176 Q R W M E R L K T V A G S K M Q G L L E R V N T E
CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTTGTGGAGCGCGTGAACACGG 2250

2251 I H F V T K C A F Q P P P S C L R F V Q T N I S R
AGATAACACTTGTCAACAAATGTGCCCTTCAGCCCCCCCCAGCTGTCTCGCTGTCCAGACCAACATCTCCC 2325

2326 L L Q E T S E Q L V A L K P W I T R Q N F S R C L
GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGCGCTGAAGCCCTGGATCACTGCCAGAACTTCTCCGGTGCC 2400

2401 E L Q C Q P D S S T L P P P W S P R P L E A T A P
TGGAGCTGCAGTGTCAAGCCGACTCCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCC 2475

2476 T A P STOP
CGACAGCCCCGTGA 2489

Figure 35B

Figure 36A

SP \leftarrow SP
 0001 ATGGATTTCAGGTGCAGATTTCAGCTTCCCTGCTAATCAGTGCCTCAGTCATAATTCAGAGGAGAGGTCAG 0075

L V E S G G G L V Q P G G S L R L S C A A S G F N
 0076 CTGGTGGAGTCTGGCGGTGGCTGGTGCAGGCCAGGGGCTCACTCCGTTGTCTGTGCAGCTTCTGGCTTCAC 0150

I K D T Y I H W V R Q A P G K G L E W V A R I Y P
 0151 ATTAAAGACACCTATATACACTGGTGCCTCAGGCCCGGTAAGGGCTGGAATGGGTTGCAAGGATTATCCT 0225

T N G Y T R Y A D S V K G R F T I S A D T S K N T
 0226 ACGAATGGTTATACTAGATATGCCATAGCGTCAAGGCCGTTCACTATAAGCGCAGACACATCCAAAAACACA 0300

A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
 0301 GCCTACCTGCAGATGAACAGCCTGCCTGCTGAGGACACTGCCGTATTATTGTTCTAGATGGGAGGGACGGC 0375

VH \leftarrow VH
 0376 TTCTATGCTATGGACTACTGGGTCAGGAACCCCTGGTCACCGTCTCTCGGCTAGCACCAAGGGCCATCGTC 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCCCTGGCACCCCTCCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCGCTGGTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACCGGTGACGGTGTCTTGAAGCTCAGGCGCCCTGACCAGCGGCTGACACCTTCCGGCTGCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGGTGCCTCCAGCAGCTGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
 0676 AACCTGAATCACAGCCAGCAACACCAAGGTGGACAAGAAACTGGTGAAGAGGCCAGCACAGGGAGGGAGG 0750

0751 TCTGCTGAAAGCAGGCTCAGCGCTCTGGCTGGAGCAATCCGGCTATGCCGCTATGCAGCCCAGTCAGGGCAGCAAGG 0825

0826 GGCCCCGCTGCGCTCTCACCGGAGCCCTGCGGCCCTACTATGCTCAGGGAGAGGGCTTCTGGCTTTTC 0900

0901 CCAGGCTCTGGGAGGCACAGGTAGGTGCCCTAACCCAGGCCCTGACACAAGGGCAGGTGCTGGCTCAG 0975

0976 ACCTGCCAAGAGCCATATCGGGAGGACCCCTGCCCTGACCTAACCCACCCAAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
 1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAACCTCCAACTCTCTCTGCAAGCCAAATCTTGTA 1125

K T H T C P P C P
 1126 CAAACTCACACATGCCACCGTGCCCAAGGTGAAGCCAGGCCAGGCCCTCCAGCTCAAGGCCAGGGACAGGTG 1200

A P
 1201 CCCCTAGAGTAGCCCTGCATTCAGGGACAGGCCAGGCCAGGGTGTGACAGCTCCACCTCCATCTCTCTCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAACTCTGGGGGACCGTCAGTCTCTCTTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGGTACATCGTGGTGGACGTGAGCCACGCCAGGGCTGAGTCAGTTCACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
 1426 TGGAGGTGCTATGCCAAGACAAGCCGGAGGAGCAGTACAACAGCACCTACCGGGTGGTCTGGCTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CGGCCCTGCCACAGGACTGGCTGAATGCCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCCA 1575

E K T I S K A K
 1576 TCGAGAAAACCATCTCCAAAGCCAAGGTGGACCCGTGGGTGCGAGGGCACATGGACAGAGGCCGGCTCGGC 1650

G Q P R E P Q V Y T
 1651 CCACCCCTGCCCTGAGAGTGACCGCTGACCAACCTCTGCTACAGGGCAGGCCAGAACACAGGTGACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCTGCCATCCGGATGAGCTGACCAAGAACAGGTCAAGCTGCCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATGCCGTGGAGTGAGCAAGGAGGAGCAAGGGCAGCCAGGAGAACAAACTACAAGACCACGCCCTCCGTGCTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGAAACGTCTTCAT 1950

CH \leftarrow Linker
 1951 GCTCCGTGATGCATGAGGCTCTGCACAACCAACTACAGCAGAAGAGCCTCTCCCTGCTCCGGTAAAGGCAGGTG 2025

Linker←|→FLex

G S G G G G S G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGGGTTCAAGAGGGCGGTGGATCTACCCAGGACTGCTCCTCCAACACAGCCCCATCTCCT 2100

D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAATCCGTGAGCTGCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCTCCAACC 2175

Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAAGGAGGAGGAGCTCTGGGGGGCTCTGGCGCTGGATGGAGCGGCTCAAGACTG 2250

A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGCTCAAGATGCAAGGCTTGCTGGAGCGCTGAACACGGAGATACTTGTCAACAAATGTGCCCTTC 2325

P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCCAGCTGCTTCGCTTCAGCCAACATCTCCGCCCTGCAGGAGACCTCCGAGCAGCTGG 2400

A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACCTCTCCGGTGCCTGGAGCTGCAGTGTCAAGCCGACTCCTCAA 2475

L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 36B

Figure 37A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGCCTGGCGCCAGCCCTGGAGCCAAACAACCTATCTCTCCCTGCTGCTGCTGAGCTCGGGACTCGT 0075

SP←→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCCTCAACACAGCCCCATCTCTCCGACTTCGCTGTCAAAATCCCTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAGATTACCCAGTCACCGTGGCCCTCAACCTGAGGACGAGGAGCTCTGCGGGCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTGTCAACAAATGTGCCTTCAGCCCCCCCCAGCTGCTCTCGCTTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGCAAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACCTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCCGGTGCCTGGAGCTGCAGTGTCAAGCCGACTCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

FLEX←→hinge
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCCAAATCTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCCCTGGGGGACCGTCAAGTCTCTCTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAG 0675

V T C V V V W D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCAAGACAAAGCCGGAGGAGCACTACAACAGCAGTACCGGTGGTCTCGTCCCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCAAAGCCAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCAATCCGGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCCAGGTCAAGCTGACCTCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGAGCCGGAGAACAACTACAAGAACACGCCCTCCCGTGTGGACTCCGACGGCTCTCTCACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGGGAACGTCTCTCATGCTCCGTGATGCACTGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K E V Q L V E S G G G L
1201 AACCAACTACACGAGAGCCTCTCCCTGTCTCCCGTAAAGAGGTTCAAGCTGGTGGAGTCTGGCGTGGCGCTG 1275

V Q P G G S L R L S C A A S G F N I K D T Y I H W
1276 GTGCAGCCAGGGGGCTCACTCCGTTGTCTGTGAGCTCTGGCTCAACATTAAGACACCTATACACTG 1350

V R Q A P G K G L E W V A R I Y P T N G Y T R Y A
1351 GTGCGTCAGGCCCGGGTAAGGGCTGGAATGGGTTGCAAGGATTATCTACGAATGGTTACTAGATATGCC 1425

D S V K G R F T I S A D T S K N T A Y L Q M N S L
1426 GATAGCGTCAAGGGCCGTTCACTATAAGCGAGACACATCCAAAACACGCTACCTGCAGATGAACAGCCTG 1500

R A E D T A V Y Y C S R W G G D G F Y A M D Y W G
1501 CGTGCCTGAGGACACTGCCGTATTATTGTCTAGATGGGAGGGACGGCTCTATGCTATGGACTACTGGGGT 1575

VH←→Linker
Q G T L V T V S S A S T K G P S V G G G G S G G G
1576 CAAGAACCCCTGGTACCGCTCCCTCGCTAGCACCAAGGGCCATCGTCGGCGTGGAGGGCTGGTGGAGGC 1650

Linker←→V_L
G S G G G G S D I Q M T Q S P S S L S A S V G D R
1651 GGTTCAAGGAGGCGCTGGATCTGACATCCAGATGACCCAGTCCCGAGCTCCCTGTCGCCCTGTGGCGATAGG 1725

V T I T C R A S Q D V N T A V A W Y Q Q K P G K A
1726 GTTACCATCACCTGCCGTGCCAGTCAGGATGTGAATACTGCTGTAGCCTGGTATCACAGAACCCAGGAAAGCT 1800
P K L L I Y S A S F L Y S G V P S R F S G S R S G
1801 CCGAAACTACTGATTTACTCGGCATCCTCCTACTCTGGAGTCCCTCTCGCTTCTGGCTCCAGATCTGGG 1875
T D F T L T I S S L Q P E D F A T Y Y C Q Q H Y T
1876 ACGGATTCACCTCTGACCATCAGCAGTCTGCAGCCGAAGACTTCGCAACTTATTACTGTCAGCAACATTATACT 1950
T P P T F G Q G T K V E I K R Stop
1951 ACTCCTCCCACGTTGGACAGGGTACCAAGGTGGAGATCAAACGTTGA 1998

Figure 37B

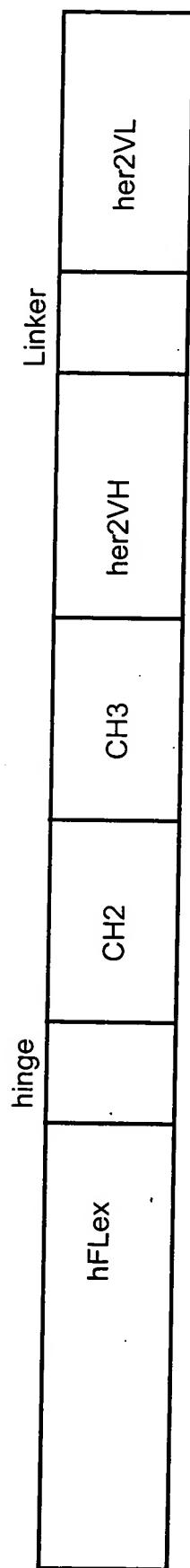


FIGURE 38

Figure 39

→SP
M T V L A P A W S P T T Y L L L L L L S S G L S
0001 ATGACAGTGCCTGGCGCCAGCCTGGAGCCAAACACCTATCTCCTCTGCTGCTGAGCTCGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCCTCCAACACAGCCCCATCCTCGACTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCGCGGGGCCCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTGTACCCAAATGTGCCCTTCAGCCCCCCCCAGCTGTCCTTCGCTTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACCTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCCTGGAGCTGCAGTGTCAAGCCGACTCTCAACCCCTGCCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

Flex←→Linker Linker←→Trailex
A T A P T A P G G G G S G G G G S G G G G G S V R E
0526 GCCACAGCCCCGACAGCCCCGGCGTGGAGGCTCTGTGGAGGCCCTCAGGAGCGGTGGATCTGTGAGAGAA 0600

R G P Q R V A A H I T G T R G R S N T L S S P N S
0601 AGAGGTCTCAGAGAGTAGCAGCTCACATAACTGGGACAGAGGAAGAACACATTGTCTCTCAAACACTCC 0675

K N E K A L G R K I N S W E S S R S G H S F L S N
0676 AAGAATGAAAAGGCTGGCCGAAATAAAACTCTGGGAATCATCAAGGAGTGGCATTCTTGAGCAAC 0750

L H L R N G E L V I H E K G F Y Y I Y S Q T Y F R
0751 TTGCACTTGAGGAATGGTAACTGGTCATCCATGAAAAGGTTTACTACATCTATTCCAAACATACTTCGA 0825

F Q E E I K E N T K N D K Q M V Q Y I Y K Y T S Y
0826 TTTCAAGGAGAAATAAAAGAAAACACAAGAACGACAACAAATGGTCAAATATATTACAAATACACAAGTTAT 0900

P D P I L L M K S A R N S C W S K D A E Y G L Y S
0901 CCTGACCCCTATATTGATGAAAAGCTAGAAATAGTTGTTGCTAAAGATGCAAGAATATGGACTCTATTCC 0975

I Y Q G G I F E L K E N D R I F V S V T N E H L I
0976 ATCTATCAAGGGGAATATTGAGCTAAGGAAATGACAGAATTGGTTCTGTAACAAATGACACTTGATA 1050

D M D H E A S F F G A F L V G Stop
1051 GACATGGACCATGAAGCCAGTTTTGGGGCTTTAGTTGGCTAA 1098

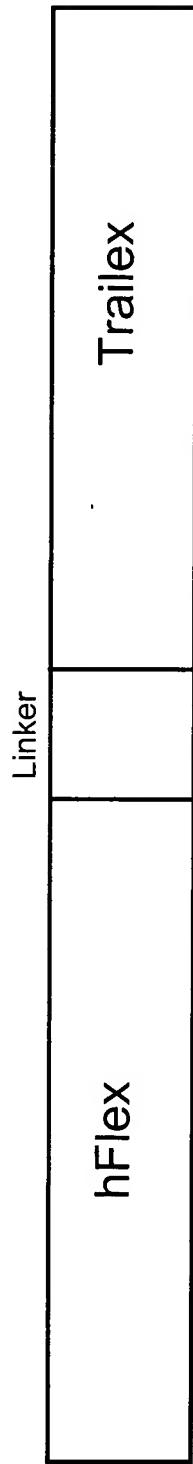


FIGURE 40

Figure 41

→SP
 M T V L A P A W S P T T Y L L L L L L L S S G L S
 0001 ATGACAGTGCTGGCGCCAGGCCATGGAGCCAAACCTATCTCTCCGTGCTGCTGCTGAGCTCGGACTCAGT 0075

SP←→FLex
 G T Q D C S F Q H S P I S S D F A V K I R E L S D
 0076 GGGACCCAGGACTGCTCCTTCAAACACAGCCCCATCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCAG 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
 0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCAAACCTGCAGGACGAGGAGCTCTGCGGGGCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
 0226 CTGGTCTGGCACAGCGCTGGATGGAGCGCTCAAAGACTGTCGCTGGTCCAAGATGCAAGGCTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
 0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCTTCAGCCCCCCCCAGCTGCTTCGCTCGCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
 0376 AACATCTCCCGCTCTGCAGGAGACCTCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACCTC 0450

S R C L E L Q C Q P D S S T L P P P P W S P R P L E
 0451 TCCCCGTGCTGGAGCTGCAGTCAGCTGCAGCCGACTCTCAACCCGCCACCCCATGGAGTCCCCGCCCTGGAG 0525

Flex←→Zipper
 A T A P T A P M K Q I E D K I E E I L S K I Y H I
 0526 GCCACAGCCCCGACAGCCCCGATGAGCAGATCGAGGACAAAATTGAGGAATCTGTCCAAGATTACACATC 0600

Zipper←→Trailex
 E N E I A R I K K L I G E T S E E T I S T V Q E K
 0601 GAGAACAGAGATCGCCGGATTAAGAAACTCATGGCAGACCTCTGAGGAAACCATTTCTACAGTTCAAGAAAAG 0675

Q Q N I S P L V R E R G P Q R V A A H I T G T R G
 0676 CAACAAAATATTCTCCCTAGTGAGAGAAAGAGGTCTCAGAGACTAGCAGCTCACATAACTGGGACAGAGGA 0750

R S N T L S S P N S K N E K A L G R K I N S W E S
 0751 AGAAGCAACACATTGTCTCTCAAACCTCAAGAATGAAAAGGCTGGGCCGAAAATAACTCTGGGAATCA 0825

S R S G H S F L S N L H L R N G E L V I H E K G F
 0826 TCAAGGAGTGGGCATTCTGAGCAACTTGCACTTGAGGAATGGTCACTGGTATCCATGAAAAGGGTTT 0900

Y Y I Y S Q T Y F R F Q E E I K E N T K N D K Q M
 0901 TACTACATCTATTCCAAACATACTTCGATTTCAAGGAGAAATAAAGAAAACACAAGAACGACAAACAAATG 0975

V Q Y I Y K Y T S Y P D P I L L M K S A R N S C W
 0976 GTCCAATATATTACAAATACACAAGTTATCTGACCCCTATATTGTTGATGAAAAGTGTAGAAATAGTTGG 1050

S K D A E Y G L Y S I Y Q G G I F E L K E N D R I
 1051 TCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGAATATTGAGCTTAAGGAAAATGACAGAATT 1125

F V S V T N E H L I D M D H E A S F F G A F L V G
 1126 TTTGTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTGGGGCTTTAGTTGGC 1200

STOP
 1201 TAA

Figure 42

→SP
 M T V L A P A W S P T T Y L L L L L L S S G L S
 0001 ATGACAGTGCTGGCCAGCCTGGAGCCAAACAACCTATCTCCTCTGCTGCTGCTGAGCTCGGACTCAGT 0075

SP←→Flex
 G T Q D C S F Q H S P I S S D F A V K I R E L S D
 0076 GGGACCCAGGACTGCTCTCAACACAGCCCCATCTCCTCGACTTCGCTGCAAAATCCGTGAGCTGTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
 0151 TACCTGCTTCAGATTACCCAGTCACCGTGGCTCAACACCTGCAGGACGAGGAGCTCTGGGGCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
 0226 CTGGTCTGACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGTCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
 0301 GTGAACACGGAGATACTTGTCAACCAATGTGCCCTTCAGCCCCCCCCAGTGTCTTCGCTTCGTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
 0376 AACATCTCCCGCTCTGCAGGAGACCTCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACITC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
 0451 TCCCGGTGCTGGAGCTGCACTGGTCAAGCCGACTCTCAACACCTGCCACCCCATGGAGTCCCGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
 A T A P T A P E P K S C D K T H T C P P C P A P E
 0526 GCCACAGCCCCGACAGCCCCGGAGCCAAATCTGTGACAAAACACTACACATGCCACCGTGCCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
 0601 CTCCCTGGGGGACCGTCACTCTCTCTCCCCAAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
 0676 GTCACATGCGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
 0751 GTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGTCTGCTCCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
 0826 CTGCACCAAGGACTGGCTGAATGCCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
 K T I S K A K G Q P R E P Q V Y T L P P S R D E L
 0901 AAAACCATCTCCAAGCCAAGGGCAAGCCAGCCCCGAGAACCCACAGGTGACACCCCTGCCCATCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
 0976 ACCAAGAACCCAGGTCAACCTGGCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
 1051 AATGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGGACTCCGACGGCTCTTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
 1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←→Trailex
 N H Y T Q K S L S L S P G K V R E R G P Q R V A A
 1201 AACCAACTACCGCAGAACAGCCTCTCCCTGTCTCCCGTAAAGTGAAGAGAAAGAGGTCTCAGAGAGTAGCAGCT 1275

H I T G T R G R S N T L S S P N S K N E K A L G R
 1276 CACATAACTGGGACCAAGAGAAGAACACACATTGTCTCTCAAACACTCCAAGAAATGAAAAGGCTCTGGCCGC 1350

K I N S W E S S R S G H S F L S N L H L R N G E L
 1351 AAAATAAAACTCCTGGGAATCATCAAGGAGTGGCATTCCTGAGCAACTTGCACTTGAGGAATGGTGAAC 1425

V I H E K G F Y Y I Y S Q T Y F R F Q E E I K E N
 1426 GTCATCCATGAAAAGGGTTTACTACATCTATTCCAACATCTTCAAGGAGGAAATAAAAGAAAAC 1500

T K N D K Q M V Q Y I Y K Y T S Y P D P I L L M K
 1501 ACAAAAGAACGACAACAAATGGCTTATATTTACAAATACACAAGTTATCCTGACCCCTATATTGATGAAA 1575

S A R N S C W S K D A E Y G L Y S I Y Q G G I F E
 1576 AGTGCTAGAAATAGTTGGTCTAAAGATGCAAGAACATGGACTCTATTCCATCTATCAAGGGGAATATTGAG 1650

L K E N D R I F V S V T N E H L I D M D H E A S F
 1651 CTTAAGGAAAATGACAGAACTTGTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTT 1725

F G A F L V G STOP
 1726 TTTGGGCCCTTTAGTTGGCTAA

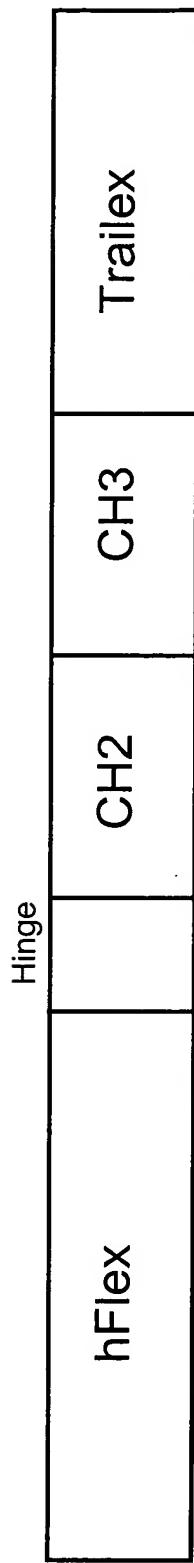


FIGURE 43

Figure 44

	HGFs+					
	SCF	G-CSF	GM-CSF	IL-3	CSF-1	
-	1	2	33	20	12	1
FL	2	22	52	65	52	12
chSM	0	3	29	22	10	0
huSM	0	2	25	26	14	1
chSM/FL	5	23	59	75	46	12
huSM/FL	3	25	56	70	50	14

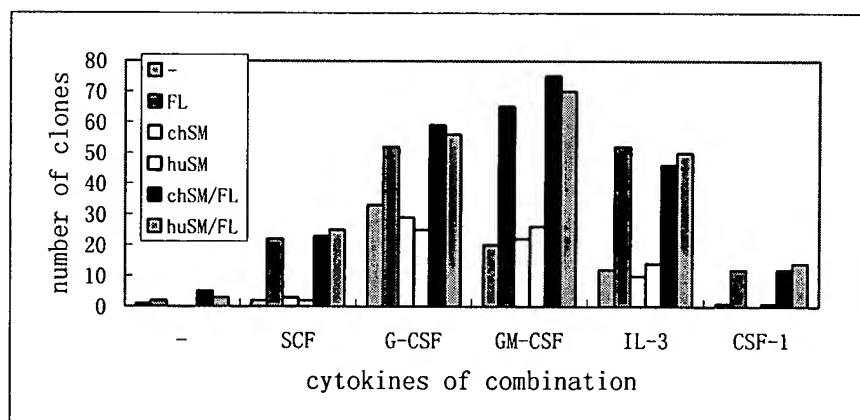
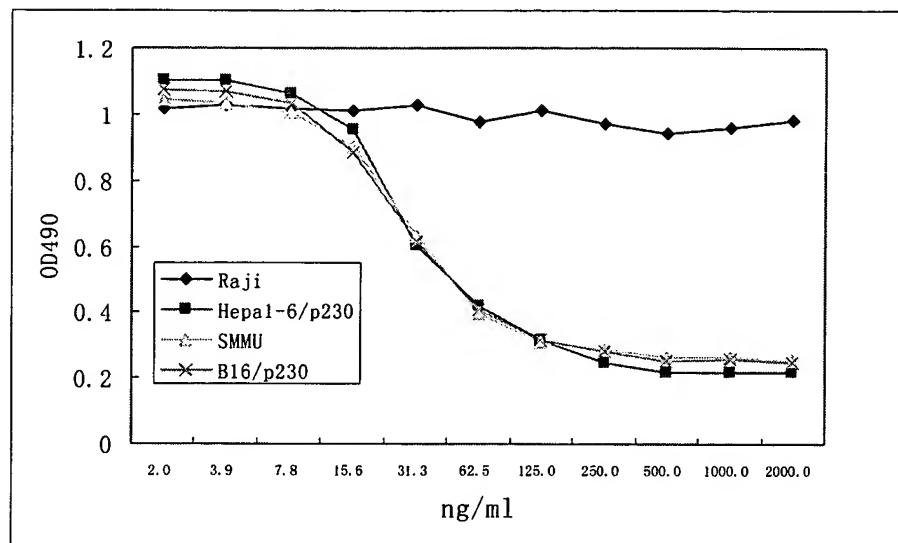
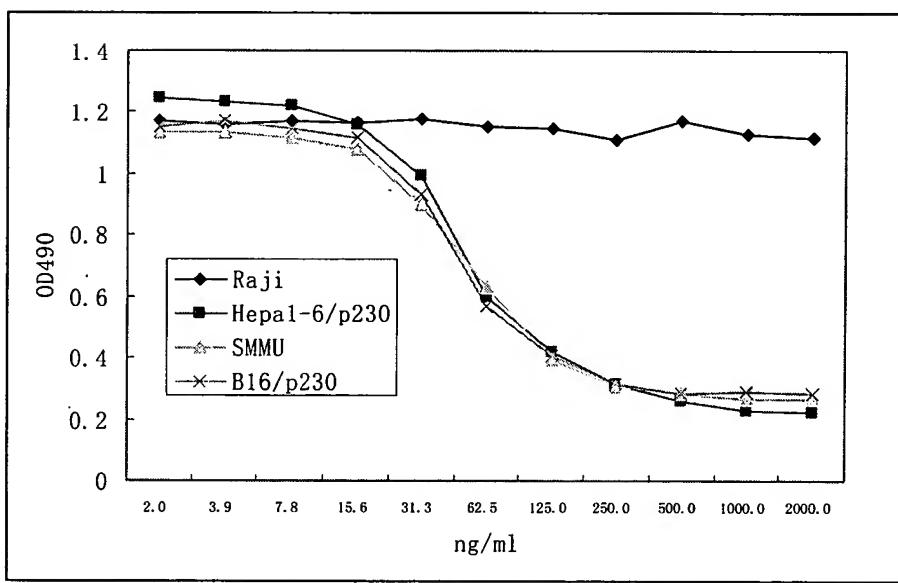


Figure 45

Item	CD3 ⁺ NK1.1 [†] (NK) (×10 ⁶)				CD3 ⁺ NK1.1 [†] (T) (×10 ⁶)				CD3 ⁺ NK1.1 [†] (NK) (×10 ⁶)				CD11c [†] (DC) (×10 ⁶)			
	Treatment	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL
spleen	0	2.0	3.0	3.5	40	38	40	7.0	6.0	6.5	3.0	3.0	3.0	2.8	2.8	2.8
	3	3.0	4.0	4.0	50	55	53	5.0	9.0	10.0	5.0	8.0	8.0	8.5	8.5	8.5
	6	6.0	5.0	5.5	76	81	82	11	18.0	18.5	35	56	56	55	55	55
	8	16	15	14	68	72	70	21	28	30	85	136	136	133	133	133
	10	17	21	23	75	80	83	17	32	31	180	189	189	182	182	182
	12	24	29	30	50	53	55	50	49	47	190	167	167	165	165	165
	15	20	18	17	38	39	40	27	33	35	180	156	156	161	161	161
	18	9	12	10	22	26	28	41	49	51	150	114	114	109	109	109
liver	0	1.0	1.0	0.9	1.0	1.3	1.1	5.0	4.5	4.8	2.0	3.0	3.0	3.5	3.5	3.5
	3	2.0	3.0	3.5	1.5	1.8	2.0	6.0	6.9	7.0	3.0	4.5	4.5	4.3	4.3	4.3
	6	3.0	5.0	4.5	1.5	1.8	1.9	5.0	4.5	4.8	5.0	5.6	5.6	5.9	5.9	5.9
	8	13.0	12.0	11.0	1.5	1.9	2.1	9.0	9.9	9.5	5.5	3.9	3.9	3.7	3.7	3.7
	10	20	18.0	19.0	3.8	3.5	3.8	3.0	2.8	3.0	18.5	17.3	16.9			
	12	11	17.0	16.0	5.6	5.5	5.2	19	19	20	9.0	9.8	10.1			
	15	5.0	6.0	6.5	3.0	2.8	3.0	9.0	8.0	7.5	2.5	4.8	5.1			
	18	2.0	3.0	3.0	3.0	3.4	3.5	2.0	2.0	2.3	8.0	6.7	7.0			
Bone marrow	0	2.0	1.0	1.5	2.0	2.0	2.5	1.0	1.0	1.2	2.0	1.8	2.0			
	3	1.0	2.0	2.0	5.9	5.5	5.3	1.8	1.2	1.1	3.0	2.0	1.9			
	6	1.5	1.8	2.0	1.9	1.8	1.8	1.8	1.2	1.3	15.0	11.7	11.5			
	8	4.0	4.5	5.0	1.5	1.5	1.8	2.5	1.9	2.1	20	32	33			
	10	4.0	5.0	4.5	2.5	1.9	2.1	2.0	1.9	2.0	39	35	36			
	12	4.0	5.2	5.5	2.5	1.5	1.6	5.0	5.7	6.1	29	29	31			
	15	4.0	4.0	4.5	3.9	3.4	3.5	5.0	4.2	4.5	19	16	15			
	18	3.0	3.3	3.5	1.9	1.8	2.0	4.0	3.7	3.4	14	14	13			

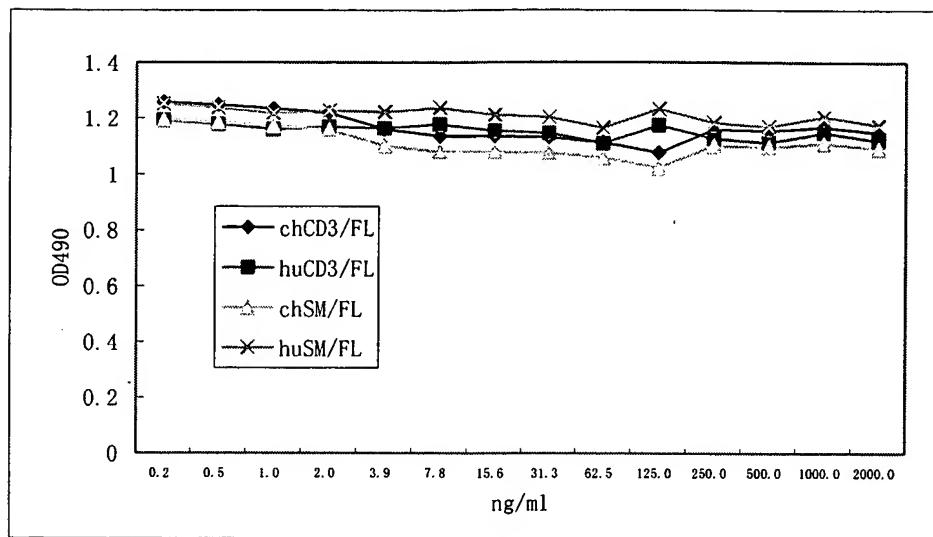
Figure 46A

chSM5-1

Figure 46B

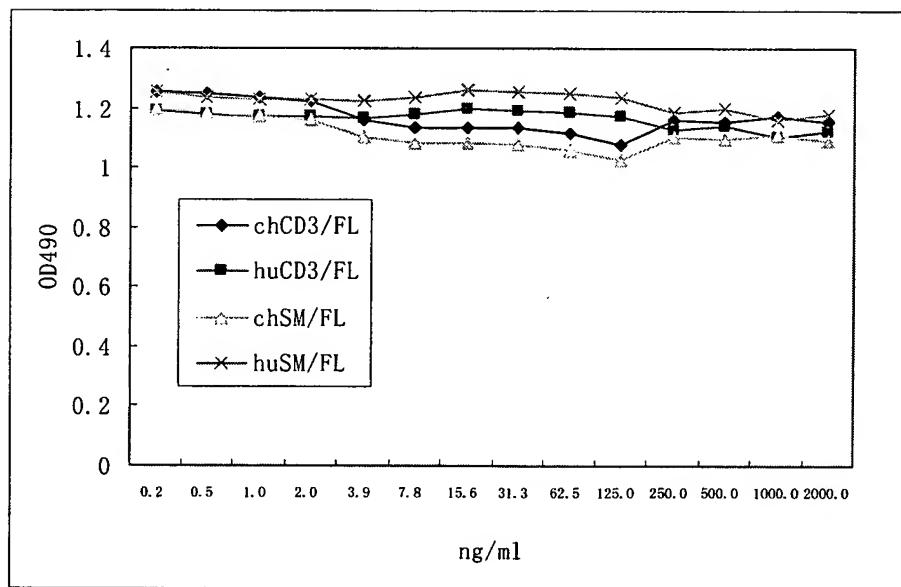
huSM5-1

Figure 47A



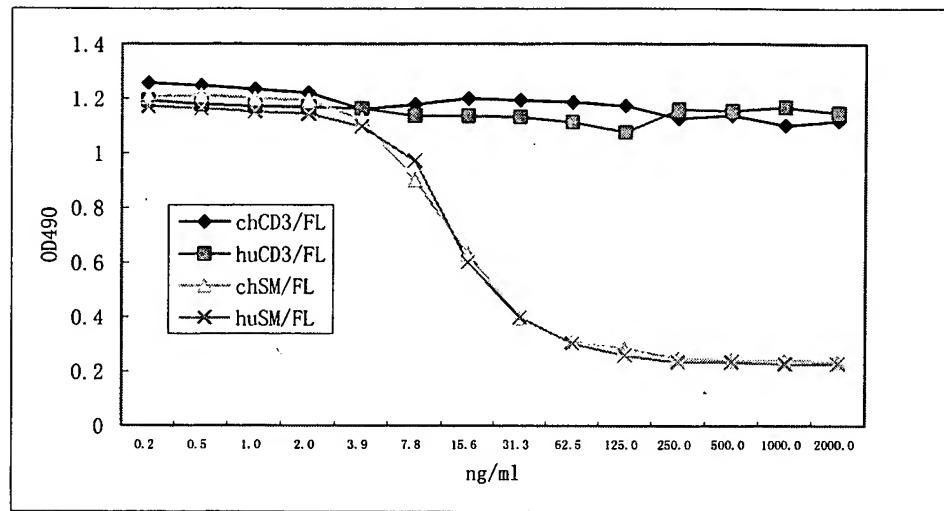
B16

Figure 47B



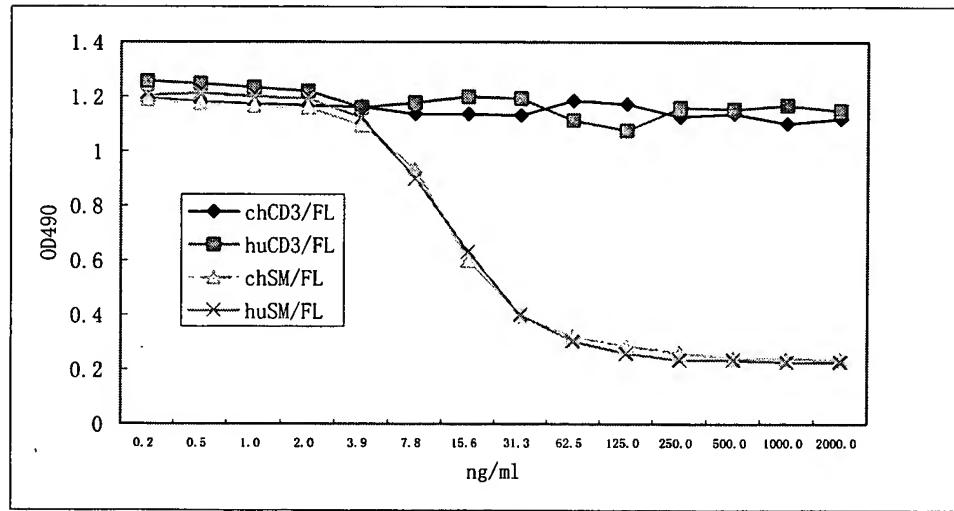
hepal-6

Figure 47C



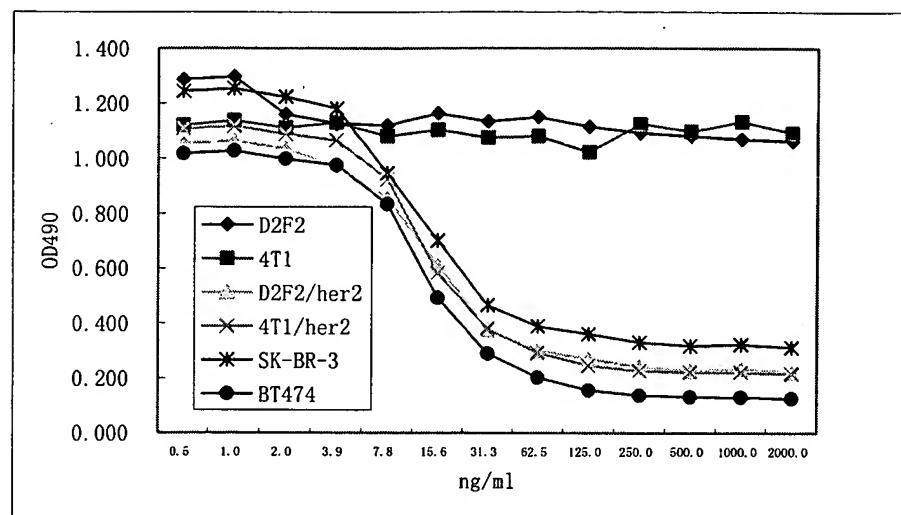
B16/p230

Figure 47D



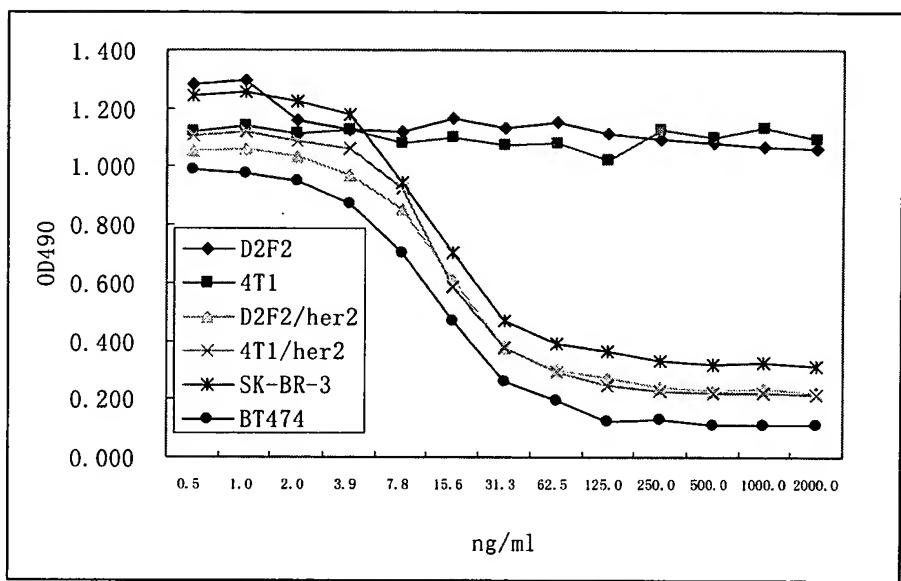
hepa1-6/p230

Figure 48A



FL/her2

Figure 48B



herceptin

Figure 49A

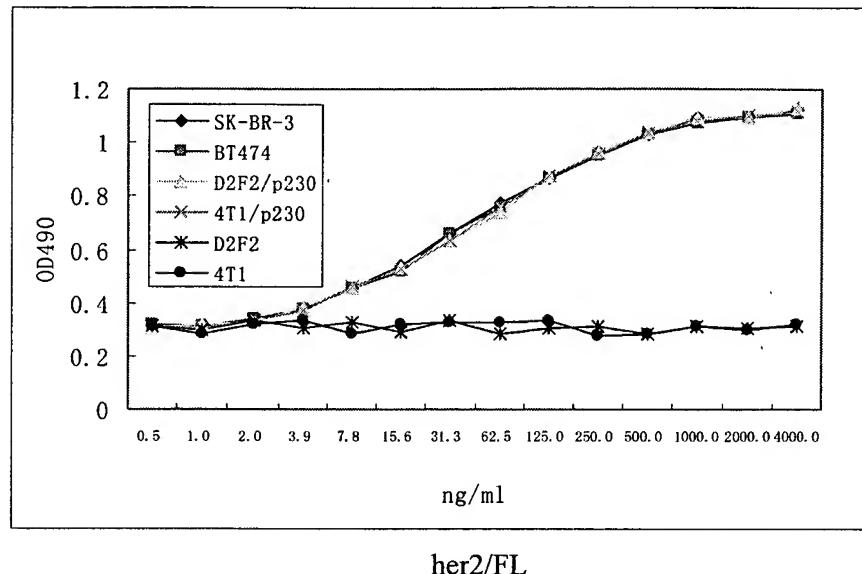


Figure 49B

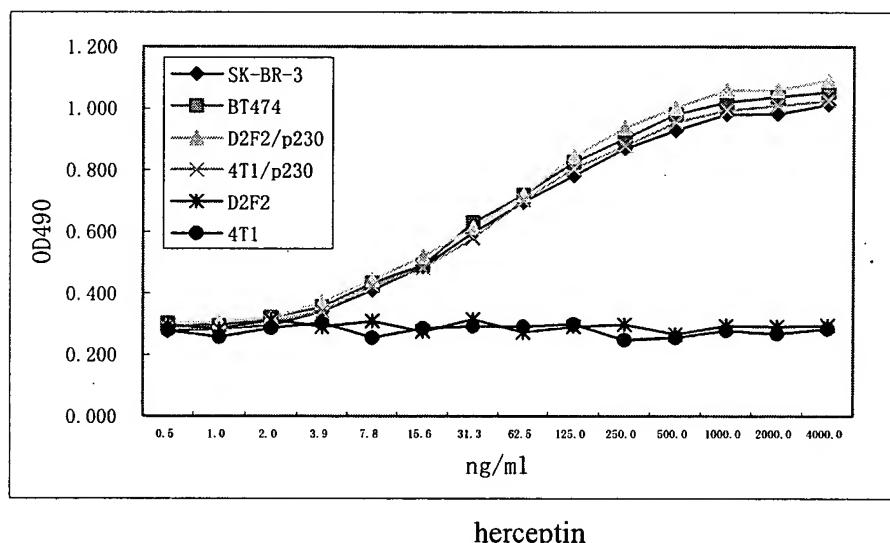


Figure 50

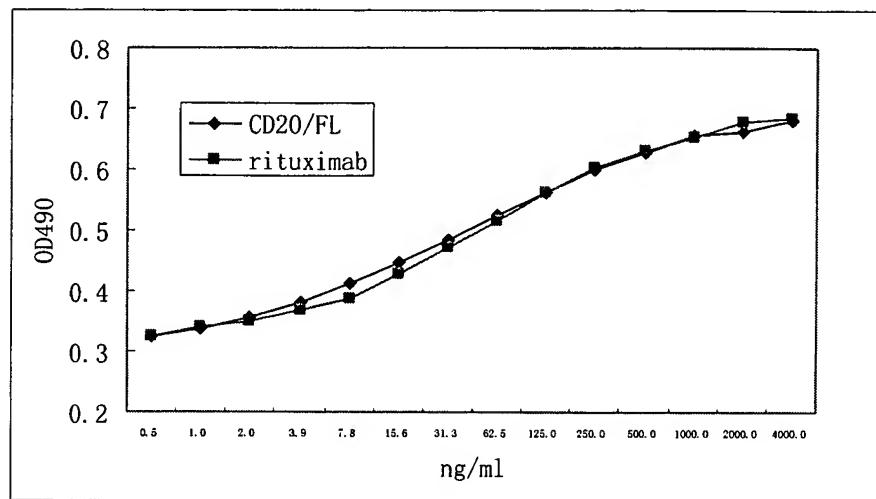


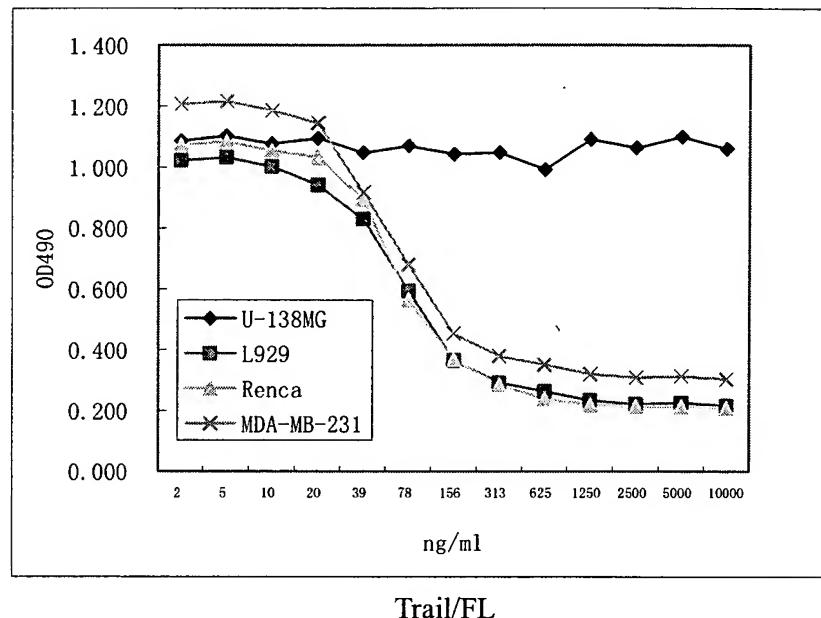
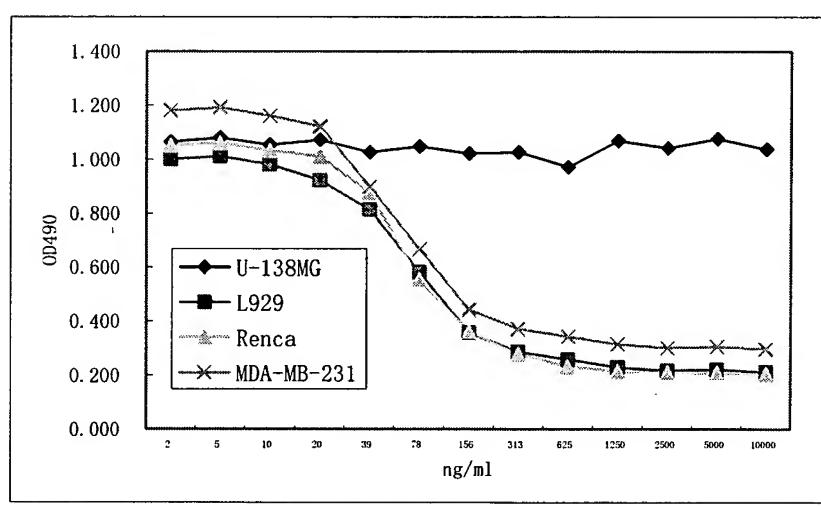
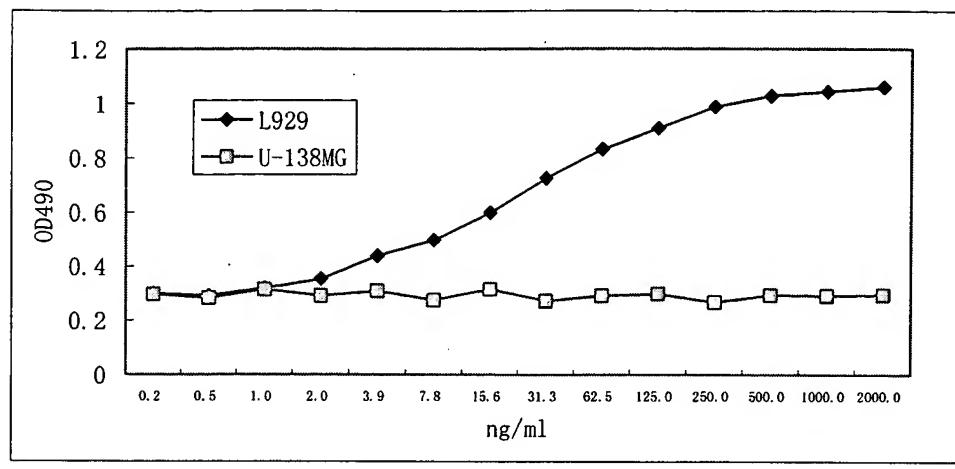
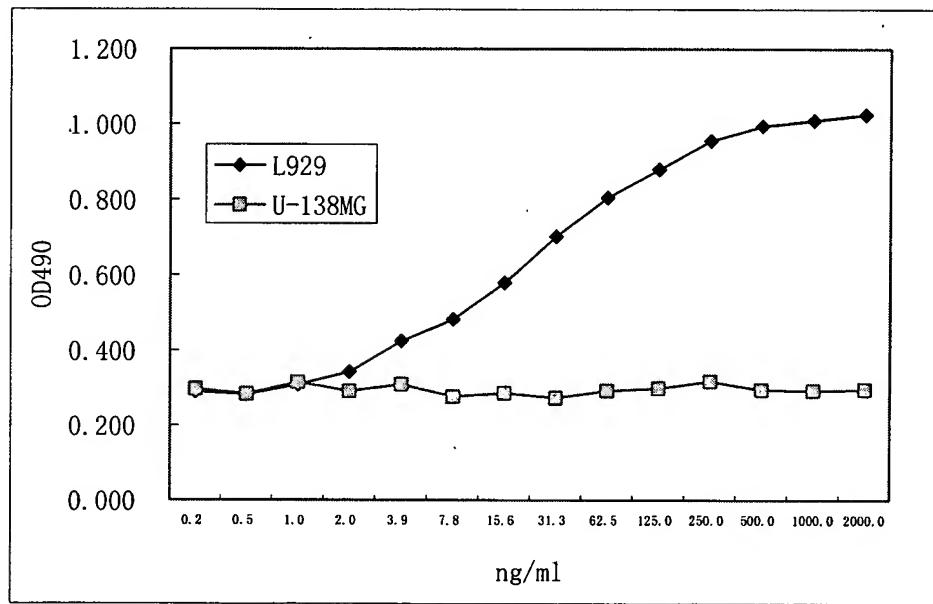
Figure 51A**Figure 51B****Trail**

Figure 52A

Trail/FL

Figure 52B

Trail

Figure 53

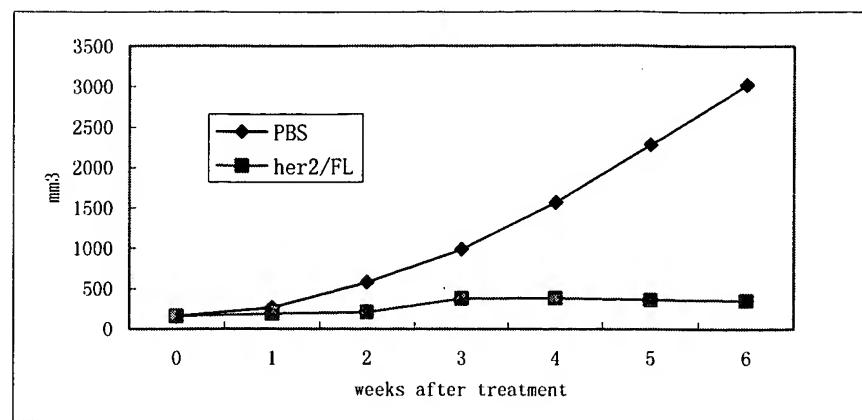


Figure 54

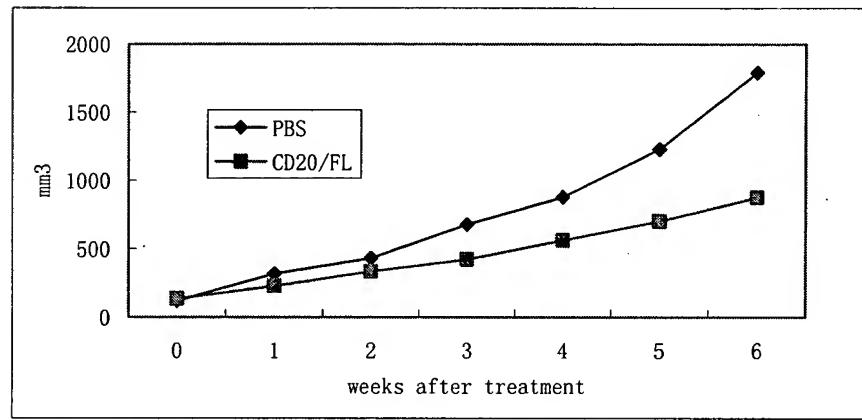
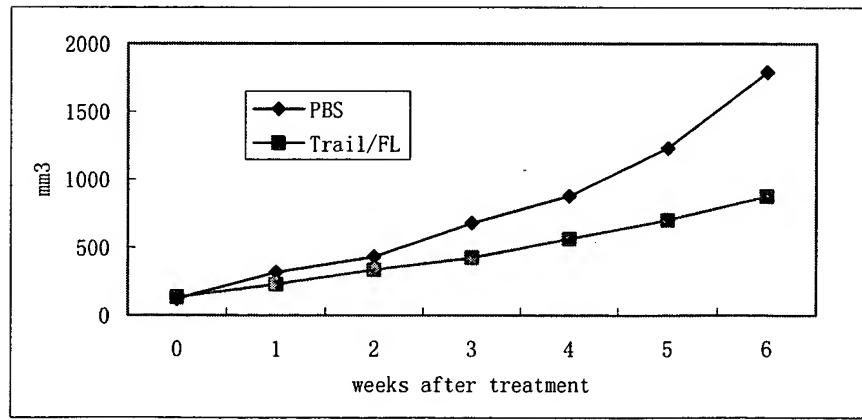


Figure 55



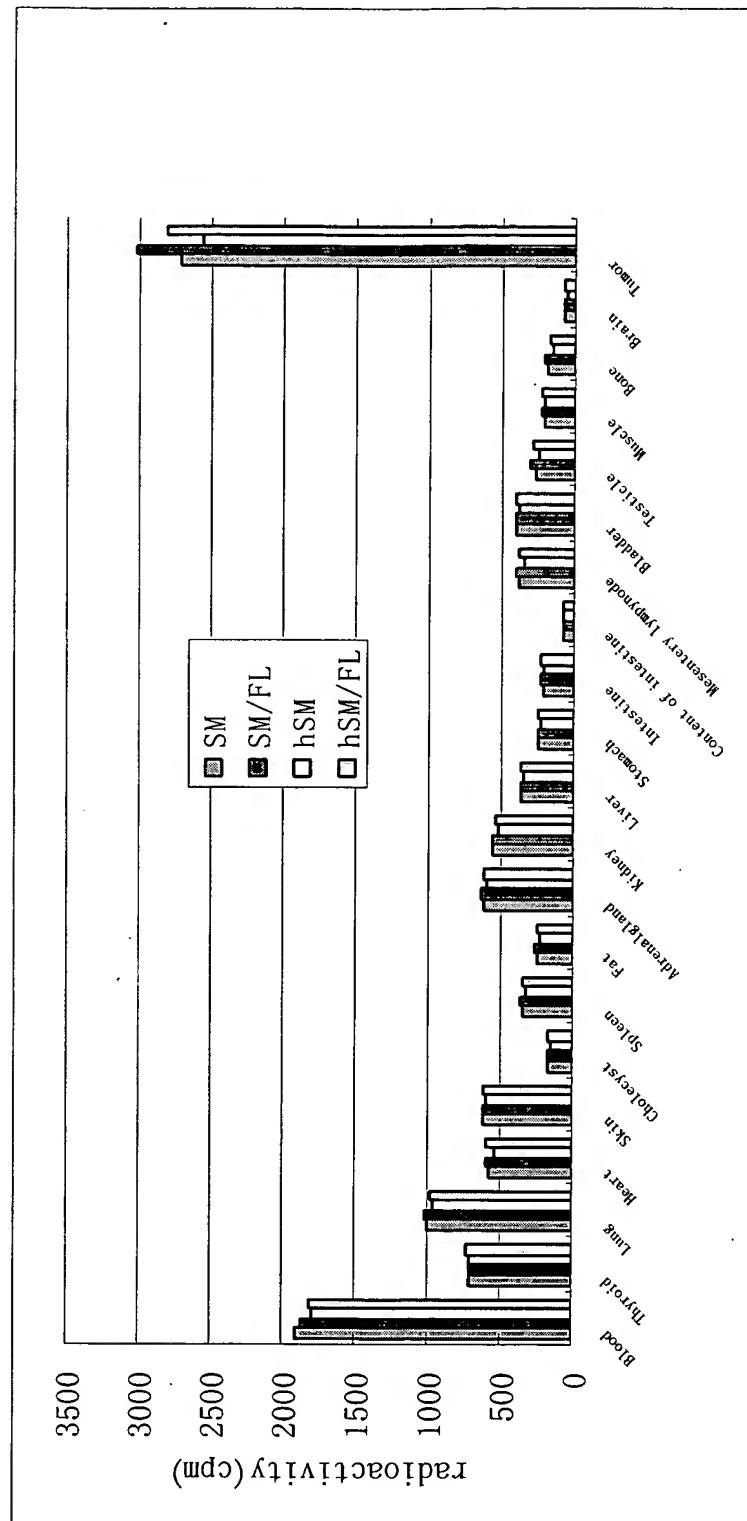


FIGURE 56

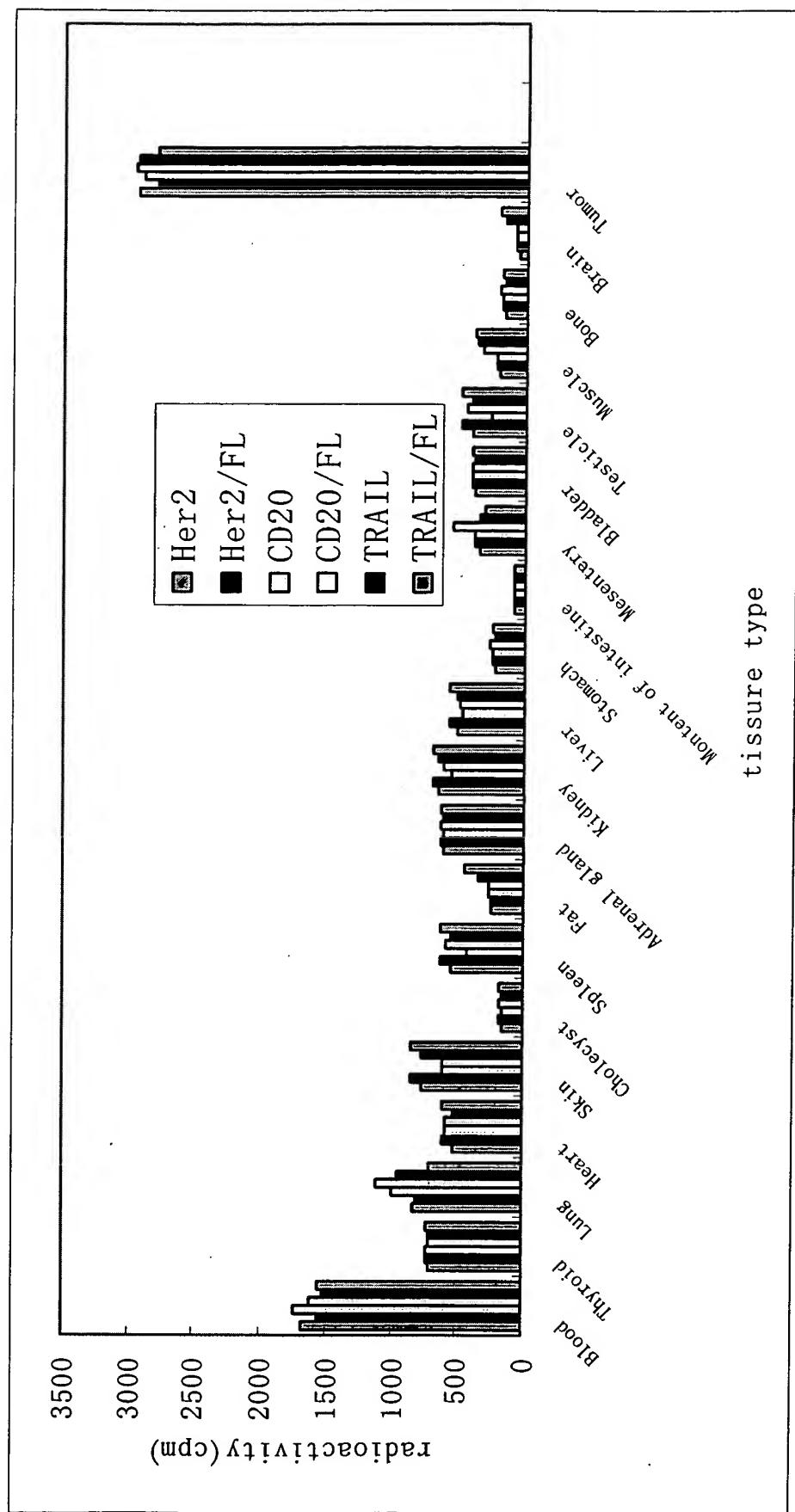


FIGURE 57